(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GGCAGAGCCT CAAGCTGACT TGGATTATGT GGTCCCTCAA ATCTACCGAC ACATGCAGGA   60

GGAGTTCCGG GGCCGGTTAG AGAGGACCAA ATCTCAGGGT CCCCTGACTG TGGCTGCTTA   120

TCAKWYGGGG AGTGTCTACT CAGCTGCTAT GGTCACAGCC CTCACCCTGT TGGCCTTCCC   180

ACTTCTGCTG TTGCATGCGG AGCGCATCAG CCTTGTGTTC CTGCTTCTGT TTCTGCAGAG   240

CTTCCTTCTC CTACATCTGC TTGCTGCTGG GATACCCGTC ACCACCCCTG GTCCTTTTAC   300

TGTGCCATGG CAGGCAGTCT CGGCTTGGGC CCTCATGGCC ACACAGACCT TCTACTCCAC   360

AGGCCACCAG CCTGTCTTTC CAGCCATCCA TTGGCATGCA GCCTTCGTGG GATTCCCAGA   420

GGGTCATGGC TCCTGTACTT GGCTGCCTGC TTTGCTAGTG GGAGCCAACA CCTTTGCCTC   480

CCACCTCCTC TTTGCAGTAG GTTGCCCACT GCTCCTGCTC TGGCCTTTCC TGTGTGAGAG   540

TCAAGGGCTG CGGAAGAGAC AGCAGCCCCC AGGGAATGAA GCTGATGCCA GAGTCAGACC   600

CGAGGAGGAA GAGGAGCCAC TGATGGAGAT GCGGCTCCGG GATGCGCCTC AGCACTTCTA   660

TGCAGCACTG CTGCAGCTGG GCCTCAAGTA CCTCTTTATC CTTGGTATTC AGATTCTGGC   720

CTGTGCCTTG GCAGCCTCCA TCCTTCGCAG GCATCTCATG GTCTGGAAAG TGTTTGCCCC   780

TAAGTTCATA TTTGAGGCTG TGGGCTTCAT TGTGAGCAGC GTGGGACTTC TCCTGGGCAT   840

AGCTTTGGTG ATGAGAGTGG ATGGTGCTGT GAGCTCCTGG TTCAGGCAGC TATTTCTGGC   900

CCAGCAGAGG TAGCCTAGTC TGTGATTACT GGCACTTGGC TACAGAGAGT GCTGGAGAAC   960

AGTGTAGCCT GGCCTGTACA GGTACTGGAT GATCTGCAAG ACAGGCTCAG CCATACTCTT   1020

ACTATCATGC AGCCAGGGGC CGCTGACATC TANGACTTCA TTATTCWATR ATTCAGGACC   1080

ACAGTGGAGT ATGATCCCTA ACTCCTGATT TGGATGCATC TGAGGGACAA GGGGGKCGGT   1140

STCCGAAGTG GAATAAAATA GGCGGGCGTG GTGACTTGCA CCT   1183

(2) INFORMATION FOR SEQ ID NO: 148:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 734 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GAATTCGGCA GAGTGAAGCA TTAGAATGAT TCCAACACTG CTCTTCTGCA CCATGAGACC   60

```
AACCCAGGGC AAGATCCCAT CCCATCACAT CAGCCTACCT CCCTCCTGGC TGCTGGCCAK      120

GATGTCGCCA GCATTACCTT CCACTGCCTT TCTCCCTGGG AAGCAGCACA GCTGAGACTG      180

GGCACCAGGC CACCTCTGTT GGGACCCACA GGAAAGAGTG TGGCAGCAAC TGCMTGGCTG      240

ACCTTTCTAT CTTCTCTAGG CTCAGGTACT GCTCCTCCAT GCCCATGGYT GGGCCGTGGG      300

GAGAAGAAGC TCTCATACGC CTTCCCACTC CCTCTGGTTT ATAGGACTTC ACTCCCTAGC      360

CAACAGGAGA GGAGGCCTCC TGGGGTTTCC CCRRGGCAGT AGGTCAAACG ACCTCATCAC      420

AGTCTTCCTT CCTCTTCAAG CGTTTCATGT TGAACACAGC TCTCTCCRCT CCCTTGTGAT      480

TTCTGAGGGT CACCACTGCC ARCCTCAGGC AACATAGAGA GCCTCCTGTT CTTTCTATGC      540

TTGGTCTGAC TGAGCCTAAA GTTGAGAAAA TGGGTGCCAA GGCCAGTGCC AGTGTCTTGG      600

GGCCCCTTTG GCTCTCCCTC ACTCTCTGAG GCTCCAGCTG GTCCTGGGAC ATGCAGCCAG      660

GACTGTGAGT CTGGGCASGT CCAAGGCCTG CACCTTCAAG AAGTGGAATA AATGTGGCCT      720

TTGCTTCTAT TTAA                                                        734
```

(2) INFORMATION FOR SEQ ID NO: 149:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1405 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
GGCACAGTGG ACCCCAGACT CCCTCTCCGC CTTTCTCTGC CTGGGGAGAC CCACTGTGTG      60

CATGGCATCA CTGACTCCCA TACCTCTGGC TATCAAAGGT TTCTGCCATG GCCACCCTGG      120

AAGSAAACCA GAGGGAGGTA GACAGGGAGA TCAGGTCCCT TCTACTCTGG TTCCTGCTCT      180

GTGAAATTGT CTCAGGCTGG CTGTGTCCAG ARGGTCCCTG GTTCTCTCAR GGATGCCAAA      240

TCTACAAGAA TCTCTCCTCT TCCAGTTCCT ATAACCTCTC CTTCCTTTTG TCTCTTTAGA      300

CCTTGGAGTA GTAGCAGCCA GGTTCTTTCT ATCTCTGGGT TAGTGCATTA TCTCTGGTGG      360

CTCCCTTACC CAGGACTTTG GGAATGGTCT TTTTGTAATA CATTCTCCTC AAATAATTCA      420

ATTTTGAGTG TTCTGTATGT ATCCTGCTGG GAGGTTGTTA TATACAAATC ACTGTGCCCG      480

TTTAGCAGAG AAGGAGACTG AAGCTCAGGG AGGTTAAGTG TCTTTCTCTA GGTCGTATTG      540

TGGAGAAAGT GGCTGACTGG GGACTTGAAT GAGGTCCCTA GTTTCATGCT CGGAGGGCAA      600

AGANGAATGT CCAATTGGCC TGAGATAAGC CTCTGGTAAA ATGTACTGTA CATAATAGGT      660

AATCAATAAA TGTTGGCTGA TGACAAACAT GTTTTCTTTG TTCATTAGTT ATAGTGATTA      720
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TGTTCTAAAT AACTCCMACA AGGAARTCAG CACATTTGGA ATATCAWTAT CTTTCCATGA        780

TAATATCTTT CCMYGGAAAG AWAATGATAT TCCMAACTGG GAGTGTCCCW AGCARATCTG        840

ANTCTGTGTA TTGGCCCTGG GGTGGGCCAG CCCCTTAGAC TCTATGGTCT CATTCTCTTT        900

GTTTACAAAA TTGAGATAAG GCCTTATTCT CTCCCCACCC CACCCATCCA TATTGTTTTG        960

AGAATAAAAT GAGAGGATGT GTGTCAAGGG TGTATTTTGG CAATAGTCTC TGAGCCATTT       1020

TCTGAGCACC TCCATACTGT TGACACTCAA GTAATATTTC ATCAGCATTC CATTCAGGNT       1080

CCTCCCTTAA TGAGGTGTGC GATGTACAAG AGTYGTGAGG TGGCAAAGGA TGGGCTCCTG       1140

AGGAAACACT TAGGAAACTG GGCTTTCTGC CATTAAAAGA GACAAACCTT TGTGGTGACC       1200

TAATTAAAGT TTTTAAAATT CAATTTGGAA AGTTAGCAAG CTAGCTCCTK TCCAGGWAAA       1260

ATAAGGAGTC AGTGCATGAC CTAACCGGTC CCGGGCTGCT TGCCATTCCA AACAACTGCA       1320

GTAAGTTTAT CACNTTCTTT CAGGGACTGA GGTTTCCAGG CACAGACTTG GATAAGGAAG       1380

GATGTCCTAT GGGGTCACAT TGATG                                           1405
```

(2) INFORMATION FOR SEQ ID NO: 150:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2890 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```
TTATATGCTA CAGCTACAGT AATTTCTTCT CCAAGCACAG AGGANCTTTC CCAGGATCAG         60

GGGGATCGCG CGTCACTTGA TGCTGCTGAC AGTGGTCGTG GGAGCTGGAC GTCATGCTCA        120

AGTGGCTCCC ATGATAATAT ACAGACGATC CAGCACCAGA GAAGCTGGGA GACTCTTCCA        180

TTCGGGCATA CTCACTTTGA TTATTCAGGG GATCCTGCAG GTTTATGGGC ATCAAGCAGC        240

CATATGGACC AAATTATGTT TTCTGATCAT AGCACAAAGT ATAACAGGCA AAATCAAAGT        300

AGAGAGAGCC TTGAACAAGC CCAGTCCCGA GCAAGCTGGG CGTCTTCCAC AGGTTACTGG        360

GGAGAAGACT CAGAAGGTGA CACAGGCACA ATAAAGCGGA GGGGTGGAAA GGATGTTTCC        420

ATTGAAGCCG AAAGCAGTAG CCTAACGTCT GTGACTACGG AAGAAACCAA GCCTGTCCCC        480

ATGCCTGCCC ACATAGCTGT GGCATCAAGT ACTACAAAGG GGCTCATTGC ACGAAAGGAG        540

GGCAGGTATC GAGAGCCCCC GCCCACCCCT CCCGGCTACA TTGGAATTCC CATTACTGAC        600

TTTCCAGAAG GGCACTCCCA TCCAGCCAGG AAACCGCCGG ACTACAACGT GGCCCTTCAG        660
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401

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AGATCGCGGA TGGTCGCACG ATCCTCCGAC ACAGCTGGGC CTTCATCCGT ACAGCAGCCA    720

CATGGGCATC CCACCAGCAG CAGGCCTGTG AACAAACCTC AGTGGCATAA AYCGAACGAG    780

TCTGACCCGC GCCTCGCCCC YTATCAGTCC CAAGGGTTTT CCACCGAGGA GGATGAAGAT    840

GAACAAGTTT CTGCTGTTTG AGGCACAGAC TTTTCTGGAA GCAGAGCGAG CCACCTGAAA    900

GGAGAGCACA AGAAGACGTC CTGAGCATTG GAGCCTTGGA ACTCACATTC TGAGGACGGT    960

GGACCAGTTT GCCTCCTTCC CTGCCTTAAA AGCAGCATGG GGSTTCTTCT CCCCTTCTTC   1020

CTTTCCCCTT TGCATGTGAA ATACTGTGAA GAAATTGCCC TGGCACTTTT CAGACTTTGT   1080

TGCTTGAAAT GCACAGTGCA GCAATCTTCG AGCTCCCACT GTTGCTGCCT GCCACATCAC   1140

ACAGTATCAT TCCAAATTCC AAGATCATCA CAACAAGATG ATTCACTCTG CTGCACTTC    1200

TCAATGCCTG GAAGGATTTT TTTTAATCTT CCTTTTAGAT TTCAATCCAG TCCTAGCACT   1260

TGATCTCATT GGGATAATGA GAAAAGCTAG CCATTGAACT ACTTGGGGCC TTTAACCCAC   1320

CAAGGAAGAC AAAGAAAAAC AATGAAATCC TTTGAGTACA GTGCTTGTCC ACTTGTTTAC   1380

AATGTCCTCC TTTTAAAAAA AAAAAAATGA GTTAAAGAT TTTGTTCAGA GAGTAAATAT    1440

ATATCCATTT AATGATTACA GTATTATTTT AAACCTTAAG TAGGGTTGCC AGCCTGGTTT   1500

CTGAAAAACC AAATATGCCG GACAGGGTGT GGCCACACCA AGAAGACGGG AAGACCTGGC   1560

TTGTGACCCT GGCTTCCCAT GTCCTTCTGG TCTCACCCGC GAAGTGCCCT ATCCTGGAAG   1620

TATGAAATGT TAGCCAATTA ATACCAAGAC ACCTCATCTG CTCCTTCCCC AGTGGATGGG   1680

GTTCTTCTGT AAAACTGTTT GCACATGGCC AGGGGAGGGA ACTAGGACCC TTGTGTCCTG   1740

TCTGAGCCTT ATGGAGGCAG GACGGTGTCA TTGGCGGATG TGTCCTGCTC CATTGAGATG   1800

GATGGCAAAC CCCATTTTTA AGTTATATTT CTTTGATTTT TGTTAATTTA GAGGTGTAGG   1860

TTTTGTTTTT TGTTTTTTTG TTTTTTTTTA AGAGAAACAT TTATAACTGG ATAGCATTGC   1920

AGTGAAAGCA GCTTGGGATG TTGGAGCTAA TGCCAGCTGT TTATACTGCT CTTTCAAGAC   1980

AGCCTCCCTT TATTGAATTG GCATTAGGGA ATAAACAAGC CTTTAAACGT GATAAAGAT    2040

CAAAAACCTG GTTAGACATG CCAGCCTTTG CAAGGCAGGT TAGTCACCAA AGACTAACCT   2100

CCAAGTGGCT TTATGGACGC TGCATATAGA GAAGGCCTAA GTGTAGCAAC CATCTGCTCA   2160

CAGCTGCTAT TAACCCTATA ATGACTGAAA TGACCCCTCC ACTCTATTTT TGTGTTGTTT   2220

TGCACAGACT CCGGAAAAGT GAAGGCTGCC AATCTGAGTA GTACTCAAAT GTGAGGAACT   2280

GCTGGTCTTG GATTTTTTTT CCATTAAATT CAGCTGATCA TATTGATCAG TAGATAAACG   2340

TAAATAGCTT CAAATTTTAA AAGTGGAATT GCAGTGTTTT TTCACTGTAT CAAACAATGT   2400

CAGTGCTTTA TTTAATAATT CTCTTCTGTA TCATGGCATT TGTCTACTTG CTTATTACAT   2460
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TGTCAATTAT GCATTTGTAA TTTTACATGT AATATGCATT ATTTGCCAGT TTTATTATAT        2520

AGGCTATGGA CCTCATGTGC ATATAGAAAG ACAGAAATCT AGCTCTACCA CAAGTTGCAC        2580

AAATGTTATC TAAGCATTAA GTAATTGTAG AACATAGGAC TGCTAATCTC AGTTCGCTCT        2640

GTGATGTCAA GTGCAGAATG TACAATTAAC TGGTGATTTC CTCATACTTT TGATACTACT        2700

TGTACCTGTA TGTCTTTTAG AAAGACATTG GTGGAGTCTG TATCCCTTTT GTATTTTTAA        2760

TACAATAATT GTACATATTG GTTATATTTT TGTTGAAGAT GGTAGAAATG TACTATGTTT        2820

ATGCTTCTAC ATCCAGTTTG TACAAGCTGG AAAATAAATA AATATAACAT AAAAAAAAAA        2880

AAAAAAAAAA                                                               2890
```

(2) INFORMATION FOR SEQ ID NO: 151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2399 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
GAACTTTTCC ATCTGGCAAA CCGGAAACTC CATCCCCATT AAACCAACTC CCCCTTTTGG         60

TTTCCCCCCC AGNGGAATAG AATTTGGACN CCCATATAAA TCCAGGAAAC CACCTAAATT        120

CTTTAGTNGT TTGTGTTTGC AAGATCTAAG GTCATGGTAA ACATTAAGTT CTTAAAATTT        180

TTGGGAGGGA CCAGTGCACC TCTCCCTCTG AATTGTTCNC CAATTTAAAA TTGGAGTAAG        240

GTTTTAAAAT GTCTNATTCC ATTGGAAGGG TNTGTTATTT CATTTTGAGC CCAGAGGGGA        300

GAGGCACATT TTAAATATCA GAATTAGATT AGCTTTGAGT TTGTACAATT GGGAACATAA        360

TAGATTTTCA TAAATTATGT GTGCCTTGTT GGAAGTGTCA ACTGTCTTTA TGTCTGCTTG        420

TAAAAGTTTC AAAATATGTT TTCCCTCAAA AAGGCAACGT TACTTCATTT GCTTGAATAT        480

TATGATAGGA ATGCTTACTG ATATTACTTG ATAGTCATAT ATAGCCTAGG AAATTTAACA        540

TATATATAAC TATAGCAGTA TTAATAATGA TAGTTGTACT TCTTTAAAAC ATTAAATTTG        600

AGGAAACTTT AATGCTGTCT CGTGTACATT GCTTTACTAC AGTGAGGGGG AATATCCTTT        660

AGATTGAGCC TCAATTTACT GGTTAGTAGT ATGTGAACTC TGGTATAAAA ACGTAAACTA        720

GACAGTAGAG CCGATGAATT AAAATTGTAA ATTGCTACAT TGGCATTTTC TACCTCCTTT        780

TCTGTCAGAG TATTACTTTT TCCAGCATTT ATTCTTATTT GTGAGTAAAG AGGAAATGGG        840

AACCTGAGGT TAAAATTGAC ATTTTTGTTT CATTGAGAAT TTAAGCAGTA GGTACAGGAG        900

AAGTGACTTG TCACATTAAT TTGGTGCCTA AATCTGTAAC TACAAGTTGT GATCGACATG        960
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                 TACAAAATGT CTAAGAAAGG TCATATGCTG AATATTTTAC TTTTCCTGTA TAGTCTGCAT      1020

          5      GATTTGTTTC ATAAACCCAG CTTATTTCCT CCAAAAAGCA AAATGGTCCT GTAATTTTTA      1080

                 AAGTAAAATA AACGTGCCAT TTTGTCTGCA ATCTATAATT TCAGGAAGTT ATTGRAAGTT      1140

                 CTGACTCAGG GCTTTTTAAC AGTTCAAGCA ATTGTCAGTT ATATTTTGGA AACTCCATCT      1200

          10     GTGTAATTCT CCAGTGCCTT GAAAGAATTA TTAACTTGGC AACACTATTA AAACTTTATA      1260

                 AAAGATGGTC TTTAGTGCAC GTGTATCATT ATATACACGT TTTAAAGTCA TATTGCTTAG      1320

          15     CTTGTTAATA ATGATTCTGC ATGTGTGCTG GGTTTGGGTA ATTCTTTAAA GGAAGTTTTC      1380

                 TAGATTTGCA CTTGATGTTT GTTTTTTAAA AACTGATTAT TTATGGCCGT GACACTGTTA      1440

                 CCAGAAAAGT AATTCTAATT AAGTTATTAT GCAAAGTCAT CTATAAGTAG CATCTGGGAA      1500

          20     GAGGAGATSG AGGCCACAGT TTGCTATTTT AGTATGAAAG GAGGATCTGT TTGGGAAACA      1560

                 TAGATTGTCT TCCCCTCAAA TGAGGGGAAA AAAAAGACC CTTTGTTCAA ATGGATTCTG      1620

          25     TTGTAAAAAA TTATTTTTAA AGGAAATCAC AAATTGTATG TCATTCTTAA TGCTAGTCTT      1680

                 ATAGAATAAA TCCATAAAAT TGTTTTTATG TTCAGTATGT TTATGTCATT CTAAATGCAG      1740

                 CAAATTCAAT GATAGCAGTT CAATTGACTC ATAGCAGTGT TTTGTATTTT TTCTAATTCT      1800

          30     TTAGCTTTCA ATATTGGATT AAAGTCTTGT TTGTGAATAT AGTTTCCGTA TGGCAAATGA      1860

                 TTTCTTGCTT ATTAGCTTTT GTTAAAGAAT GCTTAGTAAG AGCTAAGCTT TTAAAAGTAA      1920

          35     TGCAAACATT TATCGTTAAT AAAACCTATG GTGTAATATC ATATAATGCT TTTCTTTGAT      1980

                 CTTTGGAGAA TTATTCTTTT ATAGTAGTAT ACATGAATTT TGATTTTTAA AGCATTTAAA      2040

                 AACAAATCTC AATACATTAA AAAACCTGTT ATTGTTAAAA RGGAAATTAC CATGCCTTTA      2100

          40     AGAAACAAGG ATGTACATCT TCAATTCAGC ATRAGTGTCC ACATCTAGAA GGCTCTCATT      2160

                 GCAGTTGTTT ACAGTTAAGG TACCTCTATC TAAAGGGCCA AAGAAGCATT TCATAYTTTA      2220

          45     ACACCTCACA TTCTTTCAGG ATTAAGACAT ATGAAAATAG TCTGAATAGG ATAAATTTGG      2280

                 ATAGGAAGTA ACTTAACCAG TCTGGGAAGA TTCAGGCTTT TTCTATKAAA AAGCTTATTC      2340

                 CTCTTCACAA CTCNGGTGGT AGGNTTTCAT TTTTCAAGAG GGTAGATATT TTAAAGCCA       2399
          50
```

                 (2) INFORMATION FOR SEQ ID NO: 152:

          55   (i) SEQUENCE CHARACTERISTICS:
                           (A) LENGTH: 802 base pairs
                           (B) TYPE: nucleic acid
                           (C) STRANDEDNESS: double
                           (D) TOPOLOGY: linear
          60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
CGTGCCTGTA GTAAGCTCAT CCCTGCCTTT GAGATGGTGA TGCGTGCCAA GGACAATGTT      60

TACCACCTGG ACTGCTTTGC ATGTCAGCTT TGTAATCAGA GATTNTGTGT TGGAGACAAA     120

TTTTTCCTAA AGAATAACWT GAYCCTTTGC CARACGGACT ACGAGGAAGG TTTAATGAAA     180

GAAGGTTATG CACCCCMGGT TCGCTGATCT ATCAACATCA CCCCATTAAG AATACAAAGC     240

ACTACATTCT TTTATCTTTT TTGCTCCACA TGTACATAAG AATTGACACA GGAACCTACT     300

GAATAGCGTA GATATAGGAA GGCAGGATGG TTATATGGAA TAAAAGGCGG ACTGCATCTG     360

TATGTAGTGA AATTGCCCCA GTTCAGAGTT GAATGTTTAT TATTAAAGAA AAAAGTAATG     420

TACATATGGC TGGATTTTTT TGCTTGCTAT TCGTTTTTGT GTCACTTGGC ATGAGATGTT     480

TATTTTGGAC TATTGTATAT AATGTATTGT AATATTTGAA GCACAAATGT AATACAGTTT     540

TATTGTGTTA CCATTTGTGT TCCATTTGCT YCTTTGTATT GTTGCATTTA GTACAATCAG     600

TGTTTAAACT TACTGTATAT TTATGCTTTC TGTATTTACC AGCTATTTTA AATGAGCTGT     660

AACTTTCTAG TAAAGAATTG AAAAGCAAAT CCTCACTAAA GGATACACAG GATAGGATAA     720

AGCCAAGTCN CATCAACATT AAAAAATACT AAAANANAAA ACACAAAAAA AAAAAANCCC     780

GGGGGGGGCC CGGAACCCAT TC                                              802
```

(2) INFORMATION FOR SEQ ID NO: 153:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: ~461 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
CTAGGAGCAC CGAGCAGCTT GGCTAAAAGT AAGGGTGTCG TGCTGATGGC CCTGTGCGCA      60

CTGACCCGCG CTCTGCNCTC TCTGAACCTG GCGCCCCCGA CCGTCGCCGC CCCTGCCCCG     120

AGTCTGTTCC CCGCCGCCCA GATGATGAAC AATGGCCTCC TCCAACAGCC CTCTGCCTTG     180

ATGTTGCTCC CCTGCCGCCC AGTTCTTACT TCTGTGGCCC TTAATGCCAA CTTTGTGTCC     240

TGGAAGAGTC GTACCAAGTA CACCATTACA CCAGTGAAGA TGAGGAAGTC TGGGGGCCGA     300

GACCACACAG GTGGGAACAA GGACAGGGGG ATTTAAGCAG TCAAAAGGAA AAACATGTTA     360

AGACCCTAGA CTTGTATATT GACACACTTG TACCTTGTAA GGCAGAGGAA TGTAATTAAA     420

AAGCACTTAT TTGGCWNAAA AAAAAAAAAA AAAAAAAAA C                          461
```

(2) INFORMATION FOR SEQ ID NO: 154:

     (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2388 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
GCCCACGCGT CCGAAAGCGG AGAACGCTGG TGGGCCTGTT GTGGAGTACG CTTTGGACTG    60

AGAAGCATCG AGGCTATAGG ACGCAGCTGT TGCCATGACG GCCCAGGGGG GCTGGTGGCT   120

AACCGAGGCC GGCGCTTCAA GTGGGCCATT GAGCTAAGCG GGCCTGGAGG AGGCAGCAGG   180

GGTCGAAGTG ACCGGGGCAG TGGCCAGGGA GACTCGCTCT ACCCAGTCGG TTACTTGGAC   240

AAGCAAGTGC CTGATACCAG CGTGCAAGAG ACAGACCGGA TCCTGGTGGA GAAGCGCTGC   300

TGGGACATCG CCTTGGGTCC CCTCAAACAG ATTCCCATGA ATCTCTTCAT CATGTACATG   360

GCAGGCAATA CTATCTCCAT CTTCCCTACT ATGATGGTGT GTATGATGGC CTGGCGACCC   420

ATTCAGGCAC TTATGGCCAT TTCAGCCACT TTCAAGATGT TAGAAAGTTC AAGCCAGAAG   480

TTTCTTCAGG GTTTGGTCTA TCTCATTGGG AACCTGATGG GTTTGGCATT GGCTGTTTAC   540

AAGTGCCAGT CCATGGGACT GTTACCTACA CATGCATCGG ATTGGTTAGC CTTCATTGAG   600

CCCCCTGAGA GAATGGAGTT CAGTGGTGGA GGACTGCTTT TGTGAACATG AGAAAGCAGC   660

GCCTGGTCCC TATGTATTTG GGTCTTATTT ACATCCTTCT TTAAGCCCAG TGGCTCCTCA   720

GCATACTCTT AAACTAATCA CTTATGTTAA AAAGAACCAA AAGACTCTTT TCTCCATGGT   780

GGGGTGACAG GTCCTAGAAG GACAATGTGC ATATTACGAC AAACACAAAG AAACTATACC   840

ATAACCCAAG GCTGAAAATA ATGTAGAAAA CTTTATTTTT GTTTCCAGTA CAGAGCAAAA   900

CAACAACAAA AAAACATAAC TATGTAAACA AGAGAATAAC TGCTGCTAAA TCAAGAACTG   960

TTGCAGCATC TCCTTTCAAT AAATTAAATG GTTGAGAACA ATGCATAAAA AAAGTTGCAC  1020

AAGTTCCTTA TTTTCCTTAA TATTTCACTT CTATTTAATA CAAGCTGGGA CATAAAAATT  1080

CTGTTGGGGA TACCTGGGGG AAGATGTGAG AAACTAATGC TGAATTCAGC TTATACATGA  1140

TGAAAAGAAA AACCAGACAA AAGGAGCACA TAAATATGCA TACAGTGTAA CTGTTATTAT  1200

TTTAATACCC ACGATAAGGG ATTTTTGTTA GCATGTTTAG GGGGAACGAG GATTGGTGGG  1260

ATCCTTGGGG CCACAGGAAT CTGAGGCAAC GGAAGATATA TAGAGTGATC GTCCCCCTGC  1320

CGAAGGAACC TGGCAYCTGT CAAGCAGATG CTGCAGTTCA AACTTCAGCT TTTAAGATAG  1380

ATAGCTATTG AAGGCAGAGG GTCAGCAGGA GGATGTGTAT TTCTAATCTA CCCTGGTAAA  1440
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GTCATAGGTA AGACTCAAAA GCGGGATCTT ATTCAAAAGG CAGGTATTTC CTTTGTTTTC   1500

TGTCTTGAAA TAGCCCCTTC CCCTAAGGTG CATTCTCTCA AGTTTTCAGT ATTGCTTTAT   1560

5 TTGCAGTGAT TAAAAGAGAT GAGAGACTTT GGAGACAGAC AACGTAAGCA ACACATACAC   1620

ACATGAAATA CTCTAGACAG AGATGAATAT AAATCTGGCC TAATAACCAG TTTTCCATGT   1680

AACAGTGATT TTGTGTTTCG GGCTGAAGCA GTGGTTATAT TAAAAGCCAC TAATTCCCTT   1740

10 ATCCCTTTAA AAGATTTTTA CAATTCTCCA ACCACAAACA GCACTTCTAA AACTAACTTT   1800

ACTTTCTGCC CATAATTTGT TCTACATGGA AAAAAAAAAT ATTACTTTGG CCAGGGGTGT   1860

15 GTGTAAATGT GGCAGAATTC CTAGGCAGGC TGACCTTTAC AGTATGGGCC TTTAAGATAC   1920

TGGATCCTGG TTGGGCAACA AGTGTCACGC CTGAAGTTTC TGAAAACAAA TTAGAAGACT   1980

GTTGGCTTGG CTAATCTCGT AGTTCAGGGC CAAGTTTCTG TAGTCAGAAT GAAGAATAAA   2040

20 ATTGAAAGAA AAAGGGGGAA ATGCTTATAC TTGGCATTAA GTTGAATGCC TCAAGTCTTA   2100

ACTATGGCTT TGTAGATGAG GCAAAAGATT TCTTAGTGGT AAAATTTCTT CAACAGGTCA   2160

25 ATGCCAATCT GTATGCCATT TTAGTAAAGT AGGTAAGGAG AGTAGCCGCT CAGTAACTTT   2220

GGCACTAAAG AAAGAGTGTG GCTCTAGAAC TTCCAATCCC ATTGCTAGAT GTGCCCTTTA   2280

AAAGATGGTC CAGTGCTTTC AGGGAAGGAT GTTTAGCCAG TTTTCCTAGT ATTTGTTCCT   2340

30 TAAGATTTTT TGACCTGTGC TTAATAAGAC GGACGCGTGG GTCGACCC   2388

35

(2) INFORMATION FOR SEQ ID NO: 155:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 642 base pairs
40   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

45 AAAACAGACC ATTTAAAAAC TCAGACAAGA TTATATTTAA TATATTAATT ACTAAAAAGG   60

CACAAGATTA CACTGAACAT ATTAGCTACT AAAAAGGCAC TGCTAAGACA TTCAAGCAAA   120

50 TAGCTATTAC ACACTACTGC AGATTTTACA GGTTTCTAAT TCTAACATAT GTTTGAAAAA   180

TCCGTGAGTA TTCCAAAATA TATTTAATAA TGGAATATCT GCATTAATAT ACCATCCATG   240

TGTTTTTACC ATTTGCCTTA ATATTGAATA TACTGTTTAC CTCACACTAA AAAGAAAACC   300

55 AGAAGCCTTA TTTGTGATTT TGGGAGTGGA AGCTTCCATT TTTGTGTCAA AAATGAATCC   360

TGATTCTTAT GGAAATCTCT GTTATTAAGA TATTTCAAGA TGAGACAACA CTGAAGATCA   420

60 AATTGTGTTT AGTATCACTA TCTTCTCTCC TCGTTTCTCT CTTACTCCTC ATCCTCCCAG   480

407

```
AATCTACCAG TTTATGGTAG AAAGATGGGA ACCTTATTTG AATGTGTTTT TTTTTTTCCA      540

TGATGTCCAA TTTTGTTGTG GGAAAGGATT TGGATAAAAT TTTTGTTTAA ATTTTGGTAG      600

ATTTTTATCT ATACAAATTT AAATAAAATT ATGTTTTGTA AG                         642
```

(2) INFORMATION FOR SEQ ID NO: 156:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1251 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA CCCGGTTCTT       60

TGTCCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT GCACGTTTAA      120

AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAGTTGCT GTAGTCATCT ACAATAATAA      180

ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GAGCATATTA TTGCTGTCAT      240

GATAACAGAA TTGAGGGGTA AGGATATTTT GAGTTATCTG GAGAAAAACA TCTCTGTACA      300

AATGACAATA GCTGTTGGAA CTCGAATGCC ACCGAAGAAC TTCAGCCGTG GCTCTCTAGT      360

CTTCGTGTCA ATATCCTTTA TTGTTTTGAT GATTATTTCT TCAGCATGGC TCATATTCTA      420

CTTCATTCAG AAGATCAGGT ACACAAATGC ACGCGACAGG AACCAGCGTC GTCTCGGAGA      480

TGCAGCCAAG AAAGCCATCA GTAAATTGAC AACCAGGACA GTAAAGAAGG GTGACAAGGA      540

AACTGACCCA GACTTTGATC ATTGTGCAGT CTGCATAGAG AGCTATAAGC AGAATGATGT      600

CGTCCGAATT CTCCCCTGCA AGCATGTTTT CCACAAATCC TGCGTGGATC CCTGGCTTAG      660

TGAACATTGT ACCTGTCCTA TGTGCAAACT TAATATATTG AAGGCCCTGG GAATTGTGCC      720

GAATTTGCCA TGTACTGATA ACGTAGCATT CGATATGGAA AGGCTCACCA GAACCCAAGC      780

TGTTAACCGA AGATCAGCCC TCGGCGACCT CGCCGGCGAC AACTCCCTTG GCCTTGAGCC      840

ACTTCGAACT TCGGGGATCT CACCTCTTCC TCAGGATGGG GAGCTCACTC CGAGAACAGG      900

AGAAATCAAC ATTGCAGTAA CAAAAGAATG GTTTATTATT GCCAGTTTTG GCCTCCTCAG      960

TGCCCTCACA CTCTGCTACA TGATCATCAG AGCCACAGCT AGCTTGAATG CTAATGAGGT     1020

AGAATGGTTT TGAAGAAGAA AAAACCTGCT TTCTGACTGA TTTTGCCTTG AAGGAAAAAA     1080

GAACCTATTT TTGTGCATCA TTTACCAATC ATGCCACACA AGCATTTATT TTTAGTACAT     1140

TTTATTTTTT CATAAAATTG CTAATGCCAA AGCTTTGTAT TAAAAGAAAT AAATAATAAA     1200
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408

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ATAAAAAAAA AAAAACCCCG GGGGGGGCCC GGTCCCCAAT TGGCCCTATG G          1251
```

(2) INFORMATION FOR SEQ ID NO: 157:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2127 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```
CCGGCGGGAG AGGGAAGCTG CAGCGAGAGG CGCGGATCTC AGCGCGGGAG CAGTGCTTCT          60

GCGGCAGGCC CCTGAGGGAG GGAGCTGTCA GCCAGGGAAA ACCGAGAACA CCATCACCAT         120

GACAACCAGT CACCAGCCTC AGGACAGATA CAAAGCTGTC TGGCTTATCT TCTTCATGCT         180

GGGTCTGGGA ACGCTGCTCC CGTGGAATTT TTTCATGACG GCCACTCAGT ATTTCACAAA         240

CCGCCTGGAC ATGTCCCAGA ATGTGTCCTT GGTCACTGCT GAACTGAGCA AGGACGCCCA         300

GGCGTCAGCG CNCCCTGCAG CACCCTTGCC TGAGCGGAAC TCTCTCAGTG CCATCTTCAA         360

CAATGTCATG ACCCTATGTG CCATGCTGCC CCTGCTGTTA TTCACCTACC TCAACTCCTT         420

CCTGCATCAG AGGATCCCCC AGTCCGTACG GATCCTGGGC AGCCTGGTGG CCATCCTGCT         480

GGTGTTTCTG ATCACTGCCA TCCTGGTGAA GGTGCAGCTG GATGCTCTGC CCTTCTTTGT         540

CATCACCATG ATCAAGATCG TGCTCATTAA TTCATTTGGT GCCATCCTGC AGGGCAGCCT         600

GTTTGGTCTG GCTGGCCTTC TGCCTGCCAG CTRACACGGC CCCCATCATG AGTGGCCAGG         660

GCCTAGCAGG CTTCTTTGCC TCCGTGGCCA TGATCTGCGC TATTGCCAGT GGCTCGGAGC         720

TATCAGAAAG TGCCTTCGGC TACTTTATCA CAGCCTGTGC TGTKATCATT TTGACCATCA         780

TCTGTTACCT GGGCCTGCCC CGCCTGGAAT TCTACCGCTA CTACCAGCAG CTCAAGCTTG         840

AAGGACCCGG GGAGCAGGAG ACCAAGTTGG ACCTCATTAG CAAAGGAGAG GAGCCAAGAG         900

CAGGCAAAGA GGAATCTGGA GTTTCAGTCT CCAACTCTCA GCCCACCAAT GAAAGCCACT         960

CTATCAAAGC CATCCTGAAA AATATCTCAG TCCTGGCTTT CTCTGTCTGC TTCATCTTCA        1020

CTATCACCAT TGGGATGTTT CCAGCCGTGA CTGTTGAGGT CAAGTCCAGC ATCGCAGGCA        1080

GCAGCACCTG GGAACGTTAC TTCATTCCTG TGTCCTGTTT CTTGACTTTC AATATCTTTG        1140

ACTGGTTGGG CCGGAGCCTC ACAGCTGTAT TCATGTGGCC TGGGAAGGAC AGCCGCTGGC        1200

TGCCAAGCTG GNTGCTGGCC CGGCTGGTGT TTGTGCCACT GCTGCTGCTG TGCAACATTA        1260

AGCCCCGCCG CTACCTGACT GTGGTCTTCG AGCACGATGC CTGGTTCATC TTCTTCATGG        1320

CTGCCTTTGC CTTCTCCAAC GGCTACCTCG CCAGCCTCTG CATGTGCTTC GGGCCCAAGA        1380
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5   AAGTGAAGCC AGCTGAGGCA GAGACCGCAG AGCCATCATG GCCTTCTTCC TGTGTCTGGG   1440

     TCTGGCACTG GGGGCTGTTT TCTCCTTCCT GTTCCGGGCA ATTGTGTGAC AAAGGATGGA   1500

     CAGAAGGACT GCCTGCCTCC CTCCCTGTCT GCCTCCTGCC CCTTCCTTCT GCCAGGGGTG   1560

     ATCCTGAGTG GTCTGGCGGT TTTTTCTTCT AACTGACTTC TGCTTTCCAC GGCGTGTGCT   1620

10   GGGCCCGGAT CTCCAGGCCC TGGGGAGGGA GCCTCTGGAC GGACAGTGGG GACATTGTGG   1680

     GTTTGGGGCT CAGAGTCGAG GGACGGGGTG TAGCCTCGGC ATTTGCTTGA GTTTCTCCAC   1740

15   TCTTGGCTCT GACTGATCCC TGCTTGTGCA GGCCAGTGGA GGCTCTTGGG CTTGGAGAAC   1800

     ACGTGTGTCT CTGTGTATGT GTCTGTGTGT CTGCGTCCGT GTCTGTCAGA CTGTCTGCCT   1860

     GTCCTGGGGT GGCTAGGAGC TGGGTCTGAC CGTTGTATGG TTTGACCTGA TATACTCCAT   1920

20   TCTCCCCTGC GCCTCCTCCT CTGTGTTCTC TCCATGTCCC CCTCCCAACT CCCCATGCCC   1980

     AGTTCTTACC CATCATGCAC CCTGTACAGT TGCCACGTTA CTGCCTTTTT TAAAAATATA   2040

25   TTTGACAGAA ACCAGGTGCC TTCAGAGGCT CTCTGATTTA AATAAACCTT TCTTGTTTTT   2100

     TTCTCCATGG AAAAAAAAAA AAAAAAA   2127

30

     (2) INFORMATION FOR SEQ ID NO: 158:

         (i) SEQUENCE CHARACTERISTICS:
35   (A) LENGTH: 1625 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:
40
     CAAAAGATCT ATAATCAGGA CATTGTTTAT GTAAGTTGGA CAANAAAAAT TCTTCCCCTT   60

     TATGTCCACC CTTCCTATGA TTGCAAGACA AAATTTCCCT CCTTTACCTC ATCCCTATAA   120

45   CATGGGAGGC TGAGAAAAAT GAGGGGAGAT GGAACCAGAT ACAAGGAGAT CCAATAAGAG   180

     AAGCTTATTT AAATATTGTG AAATAAAGGA AGAMCCAAAG CATTTTTTTA AGTGGGGAAT   240

     CCTTTTGAAC AGTTATTATT TATCCATATT ATTAAYAACA TCTTTTCTGA CAAAATCCAT   300

50   CAGATGAAGT GTAAATGGAT AATCTTTTAA TGGATCTAAA CCTAGAAAGT TTCACTTACT   360

     GTTCATGTCC GTGTTCCAGA ATTGTGAAAT GGTGTGTGGT TTTGCTTTCC AAGTTCTTCT   420

55   CTGCCTCCTC TTAATTCTCT AATTCCATGT CTTACAGAAG AATGAGAAAT TTCTTTCTTA   480

     CTTGAGTATC ATGCTCTAAA AAACTTGGCT TCAGTCACAG AAACGCTGGC TCTCCTGTGC   540

     TTATATTGAA GCCAACTGCC TTTAATTCTT GGGCCCTCTT ATATTTTTAA GGTGCAAAAT   600
60

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     TTGAAGTCTC AGTCACCAGA CACAGGTTCT ATACAATTAA TGATGAGCTG GAGAAGTAAT        660

     ATGTAGCTAA TTTTTCAAAA GCATTGAATA TACTTTCCGG AAAGAAAACA GAAATTAAAT        720

5    ATTGCCACAT CTTGCCAGAA TCCCATCTGA CACCTTAACT TTGTCAGGTT TCCTACAACT        780

     TGCTAATCAA GTTTTATACA TTCTAAATCT CCCCAGTTTC TTTGGGGCTG GAAGATGCAA        840

     CTTCCATTTA ATAGAAACTT TGAAATCTTG GGGTAAGGGA GCAGTGGGGG GACTAGGGAG        900
10
     AAGGATAAGA AATAGAATTA TTGAAAAGCC CCCACCAGGG ACCTTCCTGG CCAGAATATG        960

     CAGAGTAATT CCTGCTGGCT TCACCTTTGA AAGTCCCTCG AAACTATGCA GATGAAACTG       1020

15   AGTCTGTTTT TGATATTGTC AGATGTATTC TACCTTGGAA GTCCCNACAC CTAAACTGGA       1080

     ATTCTTGTAT TTACATCTCC TCCACTGTCC CCCACACCAC CCCTCAATTC CTGCTGCCCC       1140

     TGCTAATGTT AAGCATTTTT CTCTTGTTAT CATCAGGTTC ACATTAAAAM CAGRTACTTA       1200
20
     CAAACTGACT TGAAGCACAG ATACTTTTAC GAATGTGATA AAATATTTTC TTAAGAAAAG       1260

     GAAAGAGGAT GTGGGTCAAA TAAAACACCG CATGGATGTT GATTGGTGAA TACTGGTGTA       1320

25   AGAAAAGGGA GCTCAGGAAT TTTTATTACT GTATTTGTAA ATGAGTTTGA AGGAATTTGT       1380

     AAATGCCACT GGTACATTTT TAAGGTGACA CATTTGCTCC TTATAAAGTT ATTAAAAATT       1440

     ACAGGGTAAG CTTAAATGAC GTTTGCCAGT AGTTTTACTT TATATAATCA ATATTGATAT       1500
30
     TGTTGCTGAA CTATGTAACT TTATGATGCA TTTTTCAGTC CCTTTTCAGA GCAAATGCTT       1560

     TTGCAATGGT AGTAATGTTT AGTTTAAATT GACTTAATAA ATTMTTACCT GAGCAAAAAA       1620

35   AAAAA                                                                   1625
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40   (2) INFORMATION FOR SEQ ID NO: 159:

         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1687 base pairs
               (B) TYPE: nucleic acid
45             (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

50   CGGGGTCACC AGTTATTAGA GGAAGTAACA CAAGGGGATA TGAGTGCAGC AGACACATTT         60

     CTGTCCGATC TGCCAAGGGA TGATATCTAT GTGTCAGATG TTGAGGACGA CGGTGATGAC        120

     ACATCTCTGG ATAGTGACCT GGATCCAGAG GAGCTGGCAG GAGTCAGGGG ACATCAGGGT        180
55
     CTAAGGGACC AAAAGCGTAT GCGACTTACT GAAGTGCAAG ATGATAAAGA GGAGGAGGAG        240

     GAGGAGAATC CACTGCTGGT ACCACTGGAG GAAAAGGCAG TACTGCAGGA AGAACAAGCC        300

60   AACCTGTGGT TCTCAAAGGG CAGCTTTGCT GGGNATCGAG GACGATGCCG ATGAAGGCCC        360
```

TGGAGATCAG TCAGGCCCAG CTGTTATTTG AGAACCGGYG GAAGGGACGG CAGCAGCAGC   420

AGAAGCAGCA GCTGCCACAG ACACCCCCTT CCTGTTTGAA GACTGAGATA ATGTCTCCCC   480

TGTACCAAGA TGAAGCCCCT AAGGNAACAG AGGCTTCTTC GGGGACAGAA GCTGCCACTG   540

GCCTTGAAGG GGAAGAAAAG GATGGCATCT CAGACAGTGA TAGCAGTACT AGCAKTGAGG   600

AAGAAGAGAG CTGGGAACCC TCCGTGGTAA GAAGCGAASC GTGGGCCTAA AGTCAGATGA   660

TGACGGGTTT GAGATAGTGC CTATTGAGGA CCCAGCGAAA CATCGGATAC TGGACCCCGA   720

AGGCCTTGCT CTAGGTGCTG TTATTGCCTC TTCCAAAAAG GCCAAGAGAG ACCTCATAGA   780

TAACTCCTTC AACCGGTACA CATTTAATGA GGATGAGGGG GAGCTTCCGG AGTGGTTTGT   840

GCAAGAGGAA AAGCAGCACC GGATACGACA GTTGCCTGTT GGTAAGAAGG AGGTGGAGCA   900

TTACCGGAAA CGCTGGCGGG AAATCAATGC ACGTCCCATC AAGAAGGTGG CTGAGGCTAA   960

GGCTAGAAAG AAAAGGAGGA TGCTGAAGAG GCTGGAGCAG ACCAGGAAGA AGGCAGAAGC   1020

CGTGGTGAAC ACAGTGGACA TCTNCAGAAC GAGAGAAAGT GGCACAGCTG CGAAGTCTCT   1080

ACAAGAAGGC TGGGCTTGGC AAGGAGAAAC GCCATGTCAC CTACGTTGTA GCCAAAAAAG   1140

GTGTGGGCCG CAAAGTGCGC CGGCCAGCTG GAGTCAGAGG TCATTTCAAG GTGGTGGACT   1200

CAAGGATGAA GAAGGACCAA AGAGCACAGC AACGTAAGGA ACAAAAGAAA AAACACAAAC   1260

GGAAGTAAGC AGAGCTGCCA GGCTCCCAGG AGAGCATGGG GACTAGGAGG AAGGGTGTGG   1320

CATGGCTCAG TCTGGCCCCC TTGATTACCG GCCTAGCCCC TGCTCACATC ACAGCTGTCT   1380

GAAGAACAGT GAGGTGGAGT GCCTAGAACT CCCGTGGTGG TCCTGAGCAG AGAGGAGGAT   1440

GTCCTCCTGC CTGCCTGAAG GTCTCCCATG AAAACACTGC TGAACTGTGT TGACACTCAT   1500

GACCCTTTTT TTAAACCGTT AAAGGGAAGT TCGGTGTTGG AGCGATACTC AATGTAGTCA   1560

GTCTACACCT GGACGTGTGG GCCACTTAAG CCCTCCCCAC CCCCATCCTA TTCCTRAATA   1620

AAACCAGGAT AATGGAARAA AAAAAAAAAA AAAAAAAAAG GGGGGCCCN TAAAGGGNCC   1680

CANNTTT   1687

412

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GGATGACAGA TTGCGACANA GATTTGTGAC CCTTCCTGCT GAACTTCAGA GGGAGCTGAA      60

ANCAGCGTAT GATCAAAGAC AAAGGCAGGG CGAGAACAGC ACTCACCAGC AGTCAGCCAG     120

CGCATCTGTG CCCCGAGAAT CCTTTACTTC ATCTAAAGGC AGCAGTGAAA GAAAAGAAAA     180

GAAACAAGAA GAAAAAAACC ATTGGTTCAC CAAAAAGGAT TCAGAGTCCT TTGAATAACA     240

AGCTGCTTAA CAGTCCTGCA AAAACTCTGC CAGGGGCCTG TGGCAGTCCC CAGAAGTTAA     300

TTGATGGGTT TCTAAAACAT GAAGGACCTC CTGCAGAGAA ACCCCTGGAA GAACTCTCTG     360

CTTCTACTTC AGGTGTGCCA GGCCTTTCTA GTTTGCAGTC TGACCCAGCT GGCTGTGTGA     420

GACCTCCAGC ACCCAATCTA GCTGGAGCTG TTGAATTCAA TGATGTGAAG ACCTTGCTCA     480

GAGAATGGAT AACTACAATT TCAGATCCAA TGGAAGAAGA CATTCTCCAA GTTGTGAAAT     540

ACTGTACTGA TCTAATAGAA GAAAAAGATT TGGAAAAACT GGATCTAGTT ATAAAATACA     600

TGAAAAGGCT GATGCAGCAA TCGGTGGAAT CGGTTTGGAA TATGGCATTT GACTTTATTC     660

TTGACAATGT CCAGGTGGTT TTACAACAAA CTTATGGAAG CACATTAAAA GTTACATAAA     720

TATTACCAGA GAGCCTGATG CTCTCTGATA GCTGTGCCAT AAGTGCTTGT GAGGTATTTG     780

CAAAGTGCAT GATAGTAATG CTCGGAGTTT TTATAATTTT AAATTTCTTT TAAAGCAAGT     840

GTTTTGTACA TTTCTTTTCA AAAAGTGCCA AATTTGTCAG TATTGCATGT AAATAATTGT     900

GTTAATTATT TTACTGTAGC ATAGATTCTA TTTACAAAAT GTTTGTTTAT AAAGTTTTAT     960

GGATTTTTAC AGTGAAGTGT TTACAGTTGT TTAATAAAGA ACTGTATGTA TATTTGGTAC    1020

RGGCTCCTTT TKGTGAAYCC TTAAAAACTC AACTCTAGGA RGCAACTACT GTTTATTATA    1080

CTAAARGGCT GAAAAMCCTC CAGGCCAGAC TGCTAAGCTC TGAAATYCCT GAGAGGTCTC    1140

AGACCGGGAT TCTACTTGTT CCAAGAAAGG GTAAAGCTTC TAAACCATCT TATTCTTGTC    1200

TCCAAGCATG AACACAGGAG CATGTYAAGA AAATCTTTAC TACTTTCTYC CATGCGGAGA    1260

AATCTACATA TTTTGAATTA GAAACACCCT CACACCCACT TGAAGATTTT TTTCCTGGGA    1320

ACATTATGTC CCGTAGATCA GAGGTGGTGT TGTCTTTTTG CTTCTACTGG CCATTGAGAA    1380

ACTTTGATGA TAAAAAAGAA CGGTATAGAT TTTTCAAACG TATATAAAAT ATTTTTATGT    1440

TATATGTTAT GCCATAACTT TAAAATAAAA ATAGTTTAAA ATTCTATGCT AGTGGATATT    1500

TGGAACTTTT TCCTCAAACA AACACCCCAC ACTGACTTCA GCAAAACCCT AAAACTAGCT    1560

ACAGATTACT ACTACGAATG AATCATYAAG TTTTGTGTCT GCAACAATTT AGAAGCACTA    1620

AGCCCAAATA TCAGGAAATG TGTGTATGAT GGAATTTTCT AGGACAAAAC AGATCAAGAT    1680

TAAAACAGGA TCAAGGATTA ATGGTATAAA AATGGTCTAC TAAAACAGGA TCAAGGATTA    1740

AAACAGGATC AAGGATTAAT GGTATAAAAA TCTCTACTGG TTACCGGGTG GCNGGGCCAT    1800
```

ACAGGGTAGT GGTGGATGGA TAGTTTAGTT TGGNAAGGGT AA   1842

5

(2) INFORMATION FOR SEQ ID NO: 161:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 770 base pairs
10   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
15

GGCACGAGCC CTATGCTGTT CTTGTGATAA TGAGTGAGTC TCACAAGATC TGGTGGTGTT   60

ATAGGCATCT GGCATTTCCC CTGCTGACGC TCATTCTCTA TCCTGCCACC CTGGGAAGAA   120

20
GTGTCTTCTG TCATGATTGT AAGTTTCCTG AGGCCTCCCC AGCTATGTAG AACTGTGAGC   180

CAATTAAACC TCTTTTCTCT ATAAATTATC CAGTCTTATA TATTTCTTCA TAGCAGTGTG   240

AGAACAGATA ATACCGTAAA TTGGTATCAC AGAGAGTGGG GTGTTGCTAT AAACACATCT   300
25

GAAAATGTTA AAGCAAATTT GGAACTGGGT AACAGGCAAA GGCTGGAACA GTTKGAAGAA   360

CAGTTAAGAA GAAGACAGGA AAATATGAGA AATCTTGAAA CTTCCTAGAG TCTTAAAGGT   420

30
CTCAGAAGAC ATGAAGATGT GGGAAGCTTT GGAACTTCCT AGAGACTTGT TTGAATGGCT   480

TTGACCAAAA TGCTGATAGT GATATGGACA ATGAAGTCCA GGCTGAGCTT ATCCAGACAG   540

ACATAAGAAG CTCGCTGGGA ACTTGAGTAA AGATCACTCT TGCTAGGCAA AGAGACTGGT   600
35

GGCCTTTTTT CCTCTGCCCT AGAGATCTGT GGAAATCTGA ACCTGAGAGA GATGATTTAG   660

GGTATCTGGC AGAAGAAATA TCTAAGCGGC AAAACCTTCM AGAGGAAGCA GAGCATAAAC   720

40
GTTTGAAAAA TTTGCAGCCT GACNATGGGA GACCAAAGTT AAACCCAATT   770

45   (2) INFORMATION FOR SEQ ID NO: 162:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 519 base pairs
            (B) TYPE: nucleic acid
50   (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

55 GAATTCGGCA CGAGCTGAGA GGCACAGGAG CAACAGCCAG TGCCCCCTGC AGAGGACCAC   60

    TGGGGTCACA GACTTCARAC CTGATGACCT GGGCTCAGAT CCCAGCTCTG CACCTACCAG   120

    CCGTGTGACA AGGTGTCCTC TCTGAGCCTC AGTCACACAC TGCCTTAACG GTTGGGCCTC   180
60

414

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ATGGAGCTGT TTGTGAAGGT TAAATGGGAA GACATAAAGC ACTTAGCCCA GAGCCAAGGA     240

CATGCTGAAT AGGATAATGG TGGCCTCCTT TGGCGCTGTG CTGGTGCAGG TGTGCCGAGG     300

AAYTGGGCAG GGGTGACAGA TACCTCTTCT AACCTAGTTC CTTTCCAAGA ACCTAATTGG     360

TGTCTCTCCC TCCCCCAGGC AATTGGAAGG AGGAGGCTGG GCCCCAGCCC CAGAATACGG     420

GAGGTTTCTC ACCGTGGTAG GGAAATTGCT GGGTTGGGGG TGTGGGCAAC CACAGTGATC     480

GTCTCTCTGC AGGACGGATG AGGCTTTGCT GACAGAGGC                            519
```

(2) INFORMATION FOR SEQ ID NO: 163:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 753 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
GGCACGAGCG GCACGAGCAG CCAGTTGCTG ACTGGCACAT GGCCTCCAGC GTCCCGGCTG     60

GTGGGCACAC TAGAGCCGGA GGGATCTTCT TAATTGGTAA ATTGGATCTT GAAGCTTCAC     120

TGTTTAAATC TTTTCAGTGG CTTCCCTTTG TACTTAGAAA AAAATGCAAC TTCTTCTGCT     180

GGGACTCATC CGCTCACAGC CTTCCCCTCC ACCCTCTCTC TGCCTCATGC TCTGCCCCTG     240

CCTGCCATGC CTCCGATACT CACCTTTTGT ACCCCAGCAC CCGTGCCCTC TGCCCCTCGA     300

TCTTTGCCTG GCTGGTTGCT CCTCACTCAG TGTTCAGGAC AAATGCTCCT GGCCCTACCC     360

CATCTAGCCA GTCTAGCCCG GTCTTCCCTG TCTTCCCTGT TTCATTCATG GCTCTTATTG     420

TTTGTTWACT TGTGTGCTGT TGACTTTTAA CTCTCTCAGT CCCCACTGGA ATGCAAGCGA     480

TCTCCCAAGC TCCTAGAATT GTTCCTGCCT CTTCACAGGC CCTTACGCTG TGTGTGCTCG     540

TGCCGAATTC GGCACGAGGG TATGTGCACT TGCTGGTATG TATGTAGGTG TTTGCTAACA     600

CATACGTGCA CACGCAGAAT GCTTCCAGGG GACTGCACAG CCTCTAGTTC GCAGCCCCCA     660

CCCCTCCCTT TGSCCCTGCA CTCTCCCCTC TCTGAGCTGC ATTCGCATGA AAGGGTGCAN     720

GGTTCCTGAN CCCGCNAGCG NCACCTCCTG GGA                                  753
```

(2) INFORMATION FOR SEQ ID NO: 164:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1400 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GGCACAGTTT ATTAATACCT ATTATGGGAA AGTCACTTTG GTTGGCATTG AAAATTACAT   60

CATCTTTAAA GCAGTATTTG TCCCCAGATG GACTCATCAC TAGCAAAGAC TAGGTTCATT   120

GGAAGGCATA GGGTGAGAGA ATGGGAAGAT GRAGTGGAGG CGGGTTGTTA AAGTGCTGTC   180

AGTGAGTGAT TTTGTCTACT TGAATAATGG TCCATGTTTG GGGGCATATT GTGTTTCATA   240

AGAAGTGAAA GGTATTTGCA AAGTAAGCTA CAAATGACCC ATAAATCTGT TAACAACAGT   300

CCTTAATATG CAAAGATGAA AAACAAGCAT TACTGCTACC CAAAGGGAAC TGGTGCTTGG   360

TGATGTGCAG ATGGGGCTGT TGGTTAAGAG AGCTATTACA GGTTTTCTCT CTTAGGTTTC   420

ATAGGAGGTA GTTACTGAGA TGAGATTGTT TTATCTTTTT GAATACAGAT CTCTTGTCTT   480

GAGTTAGTTC TGAGGATGGG AGTAATAAAG GAGTTTTTTG TTTTTTTGTT TGTTGTTTG   540

TTTTGGCTCC TTAGTAATAC TCCTCTGACA TTTATTTCTA TTATTCTTCA AAGAAAGGAA   600

ACCAACTGAA ATGTTTGCTT TAACAAACAT TTTAATAAGT TCTCTGGGTT TTTTTTTCCC   660

CTTTTAAAAA AATTAGCATA TACCATAGCA ATAAAGAAC TAATGTTAAC TATTGTATGC   720

TACAACTTAA GTGATTTTTC TAAAGAAGCA CAATGTCATT GRAAGTATTA TTGAAAAGGA   780

TCATAGTCAC ATTGAATTTG TGAAGGCCAA AGAAATTGAA GGGAGTGATA TTTTCATTTT   840

ATGATATTCA CATATTTAGT AAATTTTGTG TACAAGAATA CCAGGCAGAG TGTTTTACCC   900

ATGGAAACAG GTTTCAGATT ACTTTGTTTT TACTGTTAGA GTCTCAAGTT TAGAAATGCT   960

AACACTTAAA TCAGTTTTTT TCTCACTATA CTTGAAGATT GTTAATATTT TGATATCTTC   1020

CTAGCTTGAT GGAATTTAAA CATATCTTCA GATCTGTGAC AGTGACAGCC AATAGGACTG   1080

ATAATATTAG CTTCAAACCA ATAATATCCA GGGTTAAAAT AAAAATCATA GTGAAAGTAC   1140

GATTGTAAAA TTATGCTATA TTAACTTTTA AGTCTGTAAT AACTTGACAT CAAAATGTTA   1200

TGTAATTACC ATAAATAATG GCTAGCGAGA ACATCTTTGG AAATTCTCAA ATTACCTTTC   1260

TTACTACACT GTTTGCAGAA TGAATGTAGA AATGATCCTG TTAGCTTTCT GAATGTTCTG   1320

TGGTTGAATG TGTTTTTGCT TAAATAAAGC TTTTGGTATT TGTTTAAATW ACAAAAAAAA   1380

AAAAAAAAAA AAAAACTCGA   1400

416

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        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CAGGCCTCAG GGCCTCTGGT GGCTCTGGCC CAGACAGTAT TTGCAGTTCT TGTGCTATGG      60

GTGGGAGTCT TCTTCCTCAA GTTTCGGCAG CTGTGCTGTG NCTGGATGGG CTGCTCCTCC     120

CAGGGCTCAA GGGCTGTGGT CCGCTCAGGG TCTCATTTCC CCAGGCCAAG TTCAAGGCAG     180

CAGCCCTTTG TGAGGCGCTC TTGGCCCTGG GCTGGAGGGA GAACTTTAAG CTTTTTTGCT     240

CACAGGGACG TGGTATGGGC CCTGGGTGCA GGTGCCCACA TTCTGCTAAT GAGAGCTTTG     300

TCTGATCAGT CCTGGGTCCA TCAGTTTGTC CATGTGTCCG CTGCCAGCC CGTCCCTTGG      360

GATCCTTCCC CTGGGGTGTA GCCTTGTTCA TTAGTATATA CTCATTCCTT CATGCTTTCC     420

TCAGCAGAAC ACTTCCACTT CTGAGGTGAG CTTTTGCCCC RTGCCCTTCC TCCACAGGTG     480

TTGCCTTTTT ATAAAGACCT GATAGCAGAA TAAATTGGTG TTTCCCTGTT GACCCAGCAC     540

CATTTCTGTG GGCCTAGAAT ATGGCCCTCA ACCCTTAGAG TGGGGCAGTG AGGGCTTGAG     600

GAGTGACCCT TCCTTTCTCA TGGTTTTAGT CATTTTGGCT GCCAGCCCTT AATGGCACAG     660

ATCTGCTGCT TCTAACAGAT GGCCAGGAGG TGACACCGAT TTCAGCCATT GCCAAGGTTA     720

GCACCCTCTC CTTTGAGCCT AGGGCCACAC TGTTCATTGT CACTTTAGGC AAGTGCCTGT     780

TTGGCTTTAA AGGTAAGCCT GCCAGCTGTG AGAAGCCTTG GTAACTGATG GACTCATTTC     840

CTGGTCCTTA AAGATGCAGC CTCTTAAGGG CTCCTTGATG GATGCCATCT CTCCTAGCCC     900

CCAGCCCTGG TGCCACTGGT GGGCAGGTTC CCATTCTTTG GGGCTGGGAG GGACAGCTTG     960

CCTGTTTCTG GTCACAAATT ACAGTCTTCT CTCCTGTACC ATTCTGTGGC TTCAGCATGG    1020

GGGCAGTAGC CTTTCATTAG TGTAGATAGT CATTCCCTGG TAGGGTGGAG GGTAAGACAT    1080

AGGGTCTGGA ACTGTTTGGG ACCTTTTGGG GATGTCCTGT GCCTCCCAGA TTCCTMGATT    1140

CTGGGAGGAG AGGCTGCCGC ATTCTGCTGC TCCTCACAGC GAGCAAAGCT GCACCCACTT    1200

ACATTCAGTA TTTTCCTGGC ACTACAAAGA GTGGGAAGGC CTGGGATTTG CTGCTGCTCC    1260

CTTAGAGCAG GGCCCCTYTT TTCAGCACTT TGGACACCTG GAGACCCAGC CCTGTTATTT    1320

AATGGTAGTG GGCAAGTGTG TGTGCATACT GTCTGCCACT GCTTTCTCCC TGCCCCATGC    1380

CAGAGAGCCC TGTCCCTGCC AGGCCCAGCC TTCTTAGCCC CAACTTGGGA ACAAAGTGCA    1440

ACATGGGATC ATGGGTTGGG GTGCTCAGGT GAGCCCTCTC TATAGTGCTT CCCTGGGCCA    1500

AGCTGACACC AGCCCCTGAG GGTGGGGTGG GACGGGTGGT GCTTAAAAGA GGAAGGGGAC    1560

CAGTGTAGCA ACTTGCCAGG GACCCCACCC CTCCCTCTCT GGGCCTGTGC AGTGAGCATG    1620

GGGATTCCCA TCAAGGGGCC TGGCACCTGT GCTAGTTACG TAGCCGCTGN TCACGCGCTC    1680
```

417

ACTCCTGACC ACATGCACGT TCCCTAGATG CAGACTGCTT TGAACTTTAA AGCTGTACAA   1740

TTTGGTTATG TTTGTGCTGA CTTAAAATAT ATTTTAATGA GGAAAAAATA ATGGAGAACC   1800

CTGGGAAGGA CCTGGTTCTT TTGCTTCTCG GGGAACTGTA AGCCCTCGCG TTCTGGGAAT   1860

CGCTCTCTGC TGCTCTTTCC TGGAAGCTAA GCCTGTCTCC ACCGCCCGAG GCCTGCGCCG   1920

GTGCTCCCGC CGCAGTTGCG TTTGCTTTGG ACCTTGCGTG CGGGGGAGGG GGTGCTCGGT   1980

CCGAGCCCGC TCCTTTCTGT ACACCTAGCG CTGCCCGCCC CGCTTGTGTC TGAGGTCGTG   2040

TATGTCAAAA ATAAAGCCGC TAGAAACGGA AAAAAAAAA AAAAAAAAA AAAAAAAAA   2100

AAACTCGAGG GGGGGCCCGT ACCCAATTAA CCCNNTATGA TCTATAAAGC GTC   2153

(2) INFORMATION FOR SEQ ID NO: 166:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1251 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

GCCCACGCGT CCGCCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG   60

GGCTACTGGC GCTTCCTGGC GCTGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCGGTG   120

ATCTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA   180

CTAGAGTTTA ACTGGCACCC AGTGCTCATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC   240

GCCATCATCG TCTACAGACT GCCGTGGACC TGGAAATGCA GCAAGCTCCT GATGAAATCC   300

ATCCATGCAG GGTTAAATGC AGTTGCTGCC ATTCTTGCAA TTATCTCTGT GGTGGCCGTG   360

TTTGAGAACC ACAATGTTAA CAATATAGCC AATATGTACA GTCTGCACAG CTGGGTTGGA   420

CTGATAGCTG TCATATGCTA TTTGTTACAG CTTCTTTCAG GTTTTTCAGT CTTTCTGCTT   480

CCATGGGCTC CGCTTTCTCT CCGAGCATTT CTCATGCCCA TACATGTTTA TTCTGGAATT   540

GTCATCTTTG AACAGTGAT TGCAACAGCA CTTATGGGAT TGACAGAGAA ACTGATTTTT   600

TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCAGAAG GTGTTTTCGT AAATACGCTT   660

GGCCTTCTGA TCCTGGTGTT CGGGGCCCTC ATTTTTTGGA TAGTCACCAG ACCGCAATGG   720

AAACGTCCTA AGGAGCCAAA TTCTACCATT CTTCATCCAA ATGGAGGCAC TGAACAGGGA   780

GCAAGAGGTT CCATGCCAGC CTACTCTGGC AACAACATGG ACAAATCAGA TTCAGAGTTA   840

AACAGTGAAG TAGCAGCAAG GAAAAGAAAC TTAGCTCTGG ATGAGGCTGG GCAGAGATCT   900

418

```
ACCATGTAAA ATGTTGTAGA GATAGAGCCA TATAACGTCA CGTTTCAAAA CTAGCTCTAC        960

AGTTTTGCTT CTCCTATTAG CCATATGATA ATTGGGCTAT GTAGTATCAA TATTTACTTT       1020

AATCACAAAG GATGGTTTCT TGAAATAATT TGTATTGATT GAGGCCTATG AACTGACCTG       1080

AATTGGAAAG GATGTGATTA ATATAAATAA TAGCAGATAT AAATTGTGGT TATGTTACCT       1140

TTATCTTGTT GAGGACCACA ACATTAGCAC GGTGCCTTGT GCAKAATAGA TACTCAATAT       1200

GTGAATATGT GTCTACTAGT AGTTAATTGG ATAAACTGGC AGCATCCCTG A               1251
```

(2) INFORMATION FOR SEQ ID NO: 167:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 882 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
GACSMTCTAG AACTATGGTC CCCCGGGACT GCAGGAATTC GGCACAGCGG CTGCGGGCGC        60

GAGGTGAGGG GCGCGAGGTT CCCAGCAGGA TGCCCCGGCT CTGCAGGAAG CTGAAGTGAG       120

AGGCCCGGAG AGGGCCCAGC CCGCCCGGGG CAGGATGACC AAGGCCCGGC TGTTCCGGCT       180

GTGGCTGGTG CTGGGGTCGG TGTTCATGAT CCTGCTGATC ATCGTGTACT GGGACAGCGC       240

AGGCGCCGCG CACTTCTACT TGCACACGTC CTTCTCTAGG CCGCACACGG GCCGCCGCT        300

GCCCACGCCC GGGCCGGACA GGGACAGGGA GCTCACGGCC GAYTCCGATG TCGACGAKTT       360

TCTGGACAAK TTTCTCAGTG CTGGCGTGAA GCAGAGTGAC YTTCCCAGAA AGGAGACGGA       420

GCAGCCGCCT GCGCCGGGGA GCATGGAGGA GAGCGTGAGA RGCTACGACT GGTCCCCGCG       480

CGAMGCCCGG CGCACCCAGA CCAGGGCCGG CAGCARGCGG ANCGGAGGAR CGTGCTGCGG       540

GGCTTCTGCG CCAAYTCCAG CCTGGCCTTC CCCACCAAGG AGCGCGCATT CRACGACATC       600

CCCAACTCGG AGCTGAGCCA CCTGATCGTG GACGACCGGC ACGGGGCCAT CTACTGCTAC       660

GTGCCCAAGG TGGCCTGCAC CAACTGGAAG CGCGTRATGA TCGTGCTGAG CGGAAGCTGT       720

GCACCGCGTG CGCCTACCGC GACCCGYTGC GNTCCCGCGC GAGCACGTGC ACAACGCCAG       780

CGCGCACTGA CTTCAACAAT TCTGGCGCCG CTACGGGAAG TCTCCCCCAC CTCATGAAGT       840

CAAGCTCAAG AATACACCAA TTCTTTCTGC GCGACCCTTC TG                         882
```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1208 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
GGGAAACTCA AAAGGATGAT GGAATGGTTG ATGGAGCCAG AGCCTAGAAG TRAAGGGATA        60

CAGAGTGAAG ATAGAGGTAT TTACGTATAT TTWAATATTA GCTTTGGAAT TACGTAGGGA       120

TTCTTAAGAA AAGATCATGA CAGGACAGCC ACATTTGGTA AAATGTCAGG GCAGCCAGTG       180

CATGGTCCTC CTGGGGCTCC TCAGTTGACG GGTTTAAATC ATTTCCTGAT CCCCCTGCCC       240

TGGTTTGAGG AATGCATACA GTACGTGAAA TGCCTGTGGT ATGAGTTGCA ATGGGCAATC       300

AACCTGGGTA AATCCAAGAT TAATGATTAG TTCTAAAGAT CCAGTTGAAG TTCTAGAGTG       360

GGAATTTTCC GTCAAGCARC TCAGCACAGC TTTATGCCTG TTCCTCTAAT AACGATAGGT       420

AACAAATAGC TGTGTKTWCA CAGCTAGGAR GATAACCAAA TCTAGAGTTC TTGARTCTCA       480

TTTAATAAAT AAKTATTATG AGTACCAACT GCATATTTCA GGCACTGCAT TTGACTCTGT       540

TAAATACTGA TYCCTTAKGA CMSCCACWTC AGAWAACMTT AATCTGTCTG ATCAATAAAC       600

AGCTTGACTT AGAGRGGTAA AATAGCTTGC CACAGGTWAC CCAATTAGTA GGTAACAGCG       660

ACAGAATAAC AGTGCAGTTA AAATCTTAGA CTGGAGACTA ATTGCATAAG TTTGAATTTC       720

AGTTCTGCTA TGTAAATTTG GGTGAGTACC TTAATTYACC TGAGTCTCGG TCTTTATATC       780

TGTAGAATGG AGCTAATGAT ATTACTTAAT TTGCTTTATG TGAGATTAAA TGTACTAATA       840

TATGTAAATC ACTTACAACA GCAꞆTTGACA TATTTGACAT ACTTAATATA TTTGCTACTA       900

ATACTATTAG CAACAGCATT CTGATTTTCC AAGTTGAAAT TCAGTGTTTT CTTTTTTACT       960

TTGCCATAAT TTACAATGTT GTGCTCTGTA AACCATAAAT TTCCCTGAGG TGTTGTCAGG      1020

TTAAAAAAAA ATCACTATGG CCCCCARNMA CTTGGAAAAT AGAAATGAGA CCAGCTTCAT      1080

CTATATTCTT TACTGCAAAT AACTTAGAAT TGTAATAGGC TAATATGTAC TGGGACTTCC      1140

AATTTGGGAA TATGACAAAA ATAATACTAT TTAGCTAAAA CATATACAGA ACTTATTTTT      1200

CCTCTGAA                                                              1208
```

(2) INFORMATION FOR SEQ ID NO: 169:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1307 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```
GGCACGAGAG AAAAGAGGTT GAGAATGTTT TCTAGCAGGC AGAATGTGCA TACATGTTTT        60

CATGARTGTC CTTTGGGTGC TGTTTCTTTT AAATCCTCTG TGCACAGGGC TCTGGCCTTT       120

ARTAAACTGT TTTTCTGTCT TACGTCATGC TGACTGGGTG CTAGGGGCTG ATTACAAAGG       180

GGAAGAGTTG AACAGACATC AGGGGCCGAT GAAACCAAAG GACTAGGAGT CAGGAGAACA       240

AGTCAGGGAT TAGGAGACAG CGGTTTGGTT TATTGTTATC CAGCTGGAGG ACTCCTAGGG       300

GCAGCAGCAG GAGGAATACC AGGGCCACGG AGGGGCAGGA GTCTCACAGT GGAGGGCAGA       360

CTCTAACAGA TGCCAGCTGA ACGCTCGCTG GCCCTGGATG TCATACGAGT TGGGGACCAG       420

AAATCTGGGC TCAGAGAACC CGTCCAGGGA GATTTGAAGC CATGGGTTAT CTTCTAGAGT       480

TGATACTGAT AATATATTTT AATTTTTATT GATGTTTAAT ACCTTCTGAA ACAGGAGGGT       540

AAGATCAGAT GGGAAGCCCY TCTGTTGAAG GATCTTGGGA ACCTTGGTGG TTTTTTTTTT       600

TTGGTTTTTT TTTTTTTGAT CGAGCTGTGG ACATCCTTCT TAATTCGATT NTGAGGATTT       660

GTTTAACTAA AAAGTTCCCA AACACAGAAA GGGCCTCCCC ACCTGCTTTG GGGAGCTGTC       720

TGTSCTGGGA GTGCCAGGCA TCCSATGGGA CCCATCACTG CCAGTGTCTG TGCCTCCCAG       780

AGGTCAGCCC TGTGTCTGCC CTGGCTCTGT CTCCTCTGTG ACAGGGCAGA GCATTTCTGG       840

TCAGTTTCTC CATGGTGCCT CCCACCCCTT TGTAAAGTGG ATGGACATGA TGGAATTCAG       900

TTGTCTCACC CTGATAGCCT GGGTGTTGAT ATTCACTTTA CCCGCACTCA GACACAGGCG       960

ACCTTGAAGC AGTTCTCGGT GTGTAGAGTC CACGTGACAG TCCCCACAGC CTCCCCAGAT      1020

AGCTGTGTGC CTGTGCGCTA CTGCTGTGCC ATTTTCCCAA CTTNGGCGTT TCACTAAATG      1080

CAGCTGATCT CTCTCTCTGT GCACTCGTGA TCCATGTTGA ACAATACATG TAGGTTCTTT      1140

TTCCACGCAA TGTAAGAACA TGATATACTG TACGTTGGAA AGCATTTACC TTATTTATAT      1200

ACCTGAATGT TCCTACTACA CAAATAAACA TATATTAAAT WCTAAAAAAA AAAAAAAAAA      1260

CTGGAGGGGG GGCCCGGTAC CCAAATCGCC GGATAGTGAT CGTAAAC                    1307
```

(2) INFORMATION FOR SEQ ID NO: 170:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1624 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
     GGCACGAGGT CGCCGCCGCG GCCGCCTGGA ATTGTGGGAG TTGTGTCTGC CACTCGGCTG        60

     CCGGAGGCGA AGGTCCCTGA CTATGGCTCC CCAGAGCCTG CCTTCATCTA GGATGGCTCC       120

 5   TCTGGGCATG CTGCTTGGGC TGCTGATGGC CGCCTGCTTC ACCTTCTGCC TCAGTCATCA       180

     GAACCTGAAG GAGTTTGCCC TGACCAACCC AGAGAAGAGC AGCACCAAAG AAACRGAGAG       240

     AAAAGAAACC AAAGCCGAGG AGGAGCTGGA TGCCGAAGTC CTGGAGGTGT TCCACCCGAC       300

10   GCATGAGTGG CAGGCCCTTC AGCCAGGGCA GGCTGTCCCT GCAGGATCCC ACGTACGGCT       360

     GAATCTTCAG ACTGGGAAA GAGAGGCAAA ACTCCAATAT GAGGACAAGT TCCGAAATAA       420

15   TTTGAAAGGC AAAAGGCTGG ATATCAACAC CAACACCTAC ACATCTCAGG ATCTCAAGAG       480

     TGCACTGGCA AAATTCAAGG AGGGGGCAGA GATGGAGAGT TCAAAGGAAG ACAAGGCAAG       540

     GCAGGCTGAG GTAAAGCGGC TCTTCCGCCC CATTGAGGAA CTGAAGAAAG ACTTTGATGA       600

20   GCTGAATGTT GTCATTGAGA CTGACATGCA GATCATGGTA CGGCTGATCA ACAAGTTCAA       660

     TAGTTCCAGC TCCAGTTTGG AAGAGAAGAT TGCTGCGCTC TTTGATCTTG AATATTATGT       720

25   CCATCAGATG GACAATGCGC AGGACCTGCT TTCCTTTGGT GGTCTTCAAG TGGTGATCAA       780

     TGGGCTGAAC AGCACAGAGC CCCTCGTGAA GGAGTATGCT GCGTTTGTGC TGGGCGCTGC       840

     CTTTTCCAGC AACCCCAAGG TCCAGGTGGA GGCCATCGAA GGGGGAGCCC TGCAGAAGCT       900

30   GCTGGTCATC CTGGCCACGG AGCAGCCGCT CACTGCAAAG AAGAAGGTCC TGTTTGCACT       960

     GTGCTCCCTG CTGCGCCACT TCCCCTATGC CCAGCGGCAG TTCCTGAAGC TCGGGGGGCT      1020

35   GCAGGTCCTG AGGACCCTGG TGCAGGAGAA GGGCACGGAG GTGCTCGCCG TGCGCGTGGT      1080

     CACACTGCTC TACGACCTGG TCACGGAGAA GATGTTCGCC GAGGAGGAGG CTGAGCTGAC      1140

     CCAGGAGATG TCCCCAGAGA AGCTGCAGCA GTATCGCCAG GTACACCTCC TGCCAGGCCT      1200

40   GTGGGAACAG GGCTGGTGCG AGATCACGGC CCACCTCCTG GCGCTGCCCG AGCATGATGC      1260

     CCGTGAGAAG GTGCTGCAGA CACTGGGCGT CCTCCTGACC ACCTGCCGGG ACCGCTACCG      1320

45   TCAGGACCCC CAGCTCGGCA GGACACTGGC CAGCCTGCAG GCTGAGTACC AGGTGCTGGC      1380

     CAGCCTGGAG CTGCAGGATG GTGAGGACGA GGGCTACTTC CAGGAGCTGC TGGGCTCTGT      1440

     CAACAGCTTG CTGAAGGAGC TGAGATGAGG CCCCACACCA GGACTGGACT GGGATGCCGC      1500

50   TAGTGAGGCT GAGGGGTGCC AGCGTGGGTG GGCTTCTCAG GCAGGAGGAC ATCTTGGCAG      1560

     TGCTGGCTTG GCCATTAAAT GGAAACCTGA AGGCCAAAAA AAAAAAAAAA AAAAAAAAA      1620

55   AAAA                                                                  1624
```

60   (2) INFORMATION FOR SEQ ID NO: 171:

422

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 2003 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```
GGCACGAGCC AGCTTGCAGG AGGAATCGGT GAGGTCCTGT CCTGAGGCTG CTGTCCGGGG    60

CCGGTGGCTG CCCTCAAGGT CCCTTCCCTA GCTGCTGCGG TTGCCATTGC TTCTTGCCTG    120

TTCTGGCATC AGGCACCTGG ATTGAGTTGC ACAGCTTTGC TTTATCCGGG CTTGTGTGCA    180

GGGCCCGGCT GGGCTCCCCA TCTGCACATC CTGAGGACAG AAAAAGCTGG GTCTTGCTGT    240

GCCCTCCCAG GCTTAGTGTT CCCTCCCTCA AAGACTGACA GCCATCGTTC TGCACGGGGC    300

TTTCTGCATG TGACGCCAGC TAAGCATAGT AAGAAGTCCA GCCTAGGAAG GGAAGGATTT    360

TGGAGGTAGG TGGCTTTGGT GACACACTCA CTTCTTTCTC AGCCTCCAGG ACACTATGGC    420

CTGTTTTAAG AGACATCTTA TTTTTCTAAA GGTGAATTCT CAGATGATAG GTGAACCTGA    480

GTTGCAGATA TACCAACTTC TGCTTGTATT TCTTAAATGA CAAAGATTAC CTAGCTAAGA    540

AACTTCCTAG GGAACTAGGG AACCTATGTG TTCCCTCAGT GTGGTTTCCT GAAGCCAGTG    600

ATATGGGGGT TAGGATAGGA AGAACTTTCT CGGTAATGAT AAGGAGAATC TCTTGTTTCC    660

TCCCACCTGT GTTGTAAAGA TAAACTGACG ATATACAGGC ACATTATGTA AACATACACA    720

CGCAATGAAA CCGAAGCTTG GCGGCCTGGG CGTGGTCTTG CAAAATGCTT CCAAAGCCAC    780

CTTAGCCTGT TCTATTCAGC GGCAACCCCA AAGCACCTGT TAAGACTCCT GACCCCCAAG    840

TGGCATGCAG CCCCCATGCC CACCGGGACC TGGTCAGCAC AGATCTTGAT GACTTCCCTT    900

TCTAGGGCAG ACTGGGAGGG TATCCAGGAA TCGGCCCCTG CCCCACGGGC GTTTTCATGC    960

TGTACAGTGA CCTAAAGTTG GTAAGATGTC ATAATGGACC AGTCCATGTG ATTTCAGTAT    1020

ATACAACTCC ACCAGACCCC TCCAACCCAT ATAACACCCC ACCCCTGTTC GCTTCCTGTA    1080

TGGTGATATC ATATGTAACA TTTACTCCTG TTTCTGCTGA TTGTTTTTTT AATGTTTTGG    1140

TTTGTTTTTG ACATCAGCTG TAATCATTCC TGTGCTGTGT TTTTTATTAC CCTTGGTAGG    1200

TATTAGACTT GCACTTTTTT AAAAAAAGGT TTCTGCATCG TGGAAGCATT TGACCCAGAG    1260

TGGAACGCGT GGCCTATGCA GGTGGATTCC TTCAGGTCTT TCCTTTGGTT CTTTGAGCAT    1320

CTTTGCTTTC ATTCGTCTCC CGTCTTTGGT TCTCCAGTTC AAATTATTGC AAAGTAAAGG    1380

ATCTTTGAGT AGGTTCGGTC TGAAAGGTGT GGCCTTTATA TTTGATCCAC ACACGTTGGT    1440

CTTTTAACCG TGCTGAGCAG AAAACAAAAC AGGTTAAGAA GAGCCGGGTG GCAGCTGACA    1500

GAGGAAGCCG CTCAAATACC TTCACAATAA ATAGTGGCAA TATATATATA GTTTAAGAAG    1560
```

GCTCTCCATT TGGCATCGTT TAATTTATAT GTTATGTTCT AAGCACAGCT CTCTTCTCCT   1620

ATTTTCATCC TGCAAGCAAC TCAAAATATT TAAAATAAAG TTTACATTGT AGTTATTTTC   1680

AAATCTTTGC TTGATAAGTA TTAAGAAATA TTGGACTTGC TGCCGTAATT TAAAGCTCTG   1740

TTGATTTTGT TTCCGTTTGG ATTTTTGGGG GAGGGGAGCA CTGTGTTTAT GCTGGAATAT   1800

GAAGTCTGAG ACCTTCCGGT GCTGGGAACA CACAAGAGTT GTTGAAAGTT GACAAGCAGA   1860

CTGCGCATGT CTCTGATGCT TTGTATCATT CTTGAGCAAT CGCTCGGTCC GTGGACAATA   1920

AACAGTATTA TCAAAGAGAA AAAAAAAAA AAAAAACTCG NGGGGGGGCC CGGTACCCAA   1980

TTCGCCCTAT AGTGAGCCNA TTC   2003

(2) INFORMATION FOR SEQ ID NO: 172:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 786 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GGCACAGCGG CACGAGAAGA CTTTGGTGTT TAAGAGATTA ATGTGTTAGC CAGAACAACT   60

CATTTCTCTA CCMGTGTGTA GTCCATTTAT CTTTAAAGAT TTTCTATTGG AATAATTTTG   120

AAATTACTTT CTTAGTTTTC TTCATTAAAA ACTAAGAAAA TGCTTTGTTT ATTATGAATT   180

GCTATTTCTC TTGATTATTA TTCTTGGAGA AAGTCTATCA GACGTAATTC TTCTGATTTG   240

CTTCTAGGCT AGAGGAAAAT GTGAAAGATG ACAAATGAAA ATTTCAAAGG TTGTCAGTAG   300

TATGACTTCT TTTATCGTTT GTCATTATCA CAAATATATC AACATAGGAC TTTTAAAAGA   360

TATTTTGTAC ATATTGGGCC TTAGTAGGAT TTTGCATGAA TTTTTTTTTT CTTTTATGCC   420

CAGAGAGAAA GAGCAAAGAA ATAACCAAGG GTGATGTACT CGTATTGAAG GTTTACCAAA   480

TAAGGACTGC TTTTATTATG AACTATAGTC TATATTCTAA GTAAATCAAT TTTTCTATTA   540

TGTGTTTTTT GTTCCTGCAG GCAAGATCTC TGAACTTTAT GCAGAGGGTT CTTTTAAAAA   600

AACAAAGTTG AATTTTTTTA TTTCTTGGAA TATTTTTTTT CATTGATTTC TCCCAAGTAG   660

AGCAGATTCA AATCTCCTTT GTACCCTATG TCTTTTTTGT TTTGCTATTA GCTCAGTATT   720

CCGTTTCTAC ATTTTCCTTT CCTAGAACCA GTCAATAAAT GACAAAAAAA AAAAAAAAA   780

ACTCGA   786

424

(2) INFORMATION FOR SEQ ID NO: 173:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1758 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```
GGGACGAGCC CTGCCCACCT CCTGCAGCCT CCTGCGCCCC GCCGAGCTGG CGGATGGAGC      60

TGCGCACGGG GAGCGTGGGC AGCCAGGCGG TGGCGCGGAG GATGGATGGG GACAGCCGAG     120

ATGGCGGCGG CGGCAAGGAC GCCACCGGGT CGGAGGACTA CGAGAACCTG CCGACTAGCG     180

CCTCCGTGTC CACCCACATG ACAGCAGGAG CGATGGCCGG GATCCTGGAG CACTCGGTCA     240

TGTACCCGGT GGACTCGGTG AAGACACGAA TGCAGAGTTT GAGTCCAGAT CCCAAAGCCC     300

AGTACACAAG TATCTACGGA GCCCTCAAGA AAATCATGCG GACCGAAGCT TCTGGAGGCC     360

CTTGCGAGGC GTCAACGTCA TGATCATGGG TGCAGGGCCR GCCCATGCCA TGTATTTTGC     420

CTGCTATGAA AACATGAAAA GGACTTTAAA TGACGTTTTC CACCACCAAG GAAACAGCCA     480

CCTAGCCAAC GGTATTTTGA AAGCGTTTGT CTGGAGTTAG AAAGTTCTCT TCTTCAACAC     540

GTCCCTCCCC AGGGTGTTCC TCCCTGTGAC CCAGCCGCCT CGACTTCGGC CCGCTTGCTC     600

ACGAATAAAG AACTCAGAGT TGTGTGTGCA ATGCACACCC AGACACACGC ACGCACACAC     660

ACGCGCGCGC ACACACATGC TTTTTTCTGT TCCCCTCCGC TTTCTGAAGC CTGGGGAGAA     720

ATCAGTGACA GAGGTGTTTT GGTTTTATTG TTATGTGGGT TTTCTTTTGT ATTTTTTTTG     780

TTTGTTTTGT TTTTAAACAT TCAAAAGCAA TTAATGATCA GACATAGGAG AAACCCTGAA     840

TAGAAACAAA ACTTTTGAAT GCTGGATTCA AAAAAAAAAA AAAGTTATCT GGACAGCTTC     900

TTTGAGACTA TTTAAAAACT GGTACAACAG GTCTCTACAA CGCCAAGATC TAACTAAGCT     960

TTAAAAGGTC AAGAAGTTTT ATGGCTGACA AAGGACTCGC GCAACGCAGA AGGCCTTTCC    1020

CACCTTAAGC TTCCGGGGAT CTGGGAATTT TACCCCCATT CTCTTCTGTT TGTCTGAGTC    1080

TCATCTCTCT GCAAGCAAGG GCTGAAATCA TTTTGTTTGG TTGTTTTGAG GGAGAGAGGC    1140

GGGGTGGGGG GGTGCAAATC TGCCAGCAGC TCTTACGTAA GGCATGTTTT ATTGGGGAGG    1200

GCTGAGCTTT TATTTTCTCC TCTCCAGTGG GGTTGGCTTT TATTGTTTCT TGTTTGGGTT    1260

TGGAATGGAA ATATGGATAG CAGCATAAAG TACTTTTATT TTGACAAAAT TCATTTTTTT    1320

CAACAATGGA GACATAGATT TGACCCACAA TAACTTCTCC CCCTCTCTTT TTACTCTGCT    1380

CAAAAAGCAT CTCTCCTCCC ATTACCCAAC CTTGGTCATA AGTGTGCCTG GCTGGTTTGC    1440

AGATATTTGT TCTGCTTTGT AAAAATTGGC CATTAGTGCA TTTATTGAGA TGATCTCTAA    1500
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     AGAGCTATGC CCTGACCTAC CCCTGATTCT ATGACATTGG GGCCCTTCTT TTGCTGAAAC    1560

 5   TGCCTTACGT AATGGTTTTA CTCCTTGAAA GAGATTTGAC GGAATCCATT TTATGCCAAG    1620

     TGCTGCCCTG CACTGTTTCT GCAATATGTG GTGTATGCTG TGGTGATCTT GCTGGGAATG    1680

     ATTATAAGTG TGTGTGTGGT GGGGGAGTGG GTATTACATG CATTGCTGAA GAGTCAAAAA    1740

10   AAAAAAAAAA AAACTCGA                                                   1758
```

15 (2) INFORMATION FOR SEQ ID NO: 174:

         (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 888 base pairs
                (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
25   CTGTTAGAAT GCCCAGTTTA CCTGGATGGC AACCCAACAG TGCTCCTGCC CACCTGCCCC      60

     TCAATCCTCC TAGAATTCAG CCCCCAATTG CCCAGTTACC AATAAAAACT TGTACACCAG     120

     CCCCAGGGAC AGTCTCAAAT GCAAATCCAC AGAGTGASMC ACCACCTCGG GTAGAATTTG     180

30   ATGACAACAA TCCCTTTAGT GAAAGTTTTC AAGAACGGGA ACGTAAGGAA CGTTTACGAG     240

     AACAGCAAGA GAGACAACGG ATCCAACTCA TGCAGGAGGT AGATAGACAA AGAGCTTTGC     300

35   AGCAGAGGAT GGAAATGGAG CAGCATGGTA TGGTGGGCTC TGAGATAAGT AGTAGTAGGA     360

     CATCTGTGTC CCAGATTCCC TTCTACAGTT CCGACTTACC TTGTGATTTT ATGCAACCTC     420

     TAGGACCCCT TCAGCAGTCT CCACAACACC AACAGCAAAT GGGGCAGGTT TTACAGCAGC     480

40   AGAATATACA ACAAGGATCA ATTAATTCAC CCTCCACCCA AACTTTCATG CAGACTAATG     540

     AGCGAGGCAG GTAGGCCCTC CTTCATTTGT TCCTGATTCA CCATCAATCC CTGTTGGAAG     600

45   CCCAAATTTT TCTTCTGTGA AGCAGGGACA TGGAAATCTT TCTGGGACCA GCTTCCAGCA     660

     GTCCCCAGTG AGGCCTTCTT TTACACCTGC TTTACCAGCA GCACCTCCAG TAGCTAATAG     720

     CAGTCTCCCA TGTGGCCAAG ATTCTACTAT AACCCATGGA CACAGTTATC CGGGATCAAC     780

50   CCAATCGCTC ATTCAGTTGT ATTCTGATAT AATCCCAGAG GAAAAAGGGN AAAAAAAARA     840

     AMAARAAARA ARAAAGGAGA TGATGATGCA GAATTCCACC AAGGCTCC                 888
```

55

(2) INFORMATION FOR SEQ ID NO: 175:

60   (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```
GGCAGAGCTA GTGTGGACTC CATCCCCCTG GAGTGGGATC ACGNCTATGA CCTCAGTCGG      60

GACCTGGAGT CTGCAATGTC CAGAGCTCTG CCCTCTGAGG ATGAAGAAGG TCAGGATGAC     120

AAAGATTTCT ACCTCCGGGG AGCTGTTGSC TTATCAGGGG ACCACAGTGC CCTAGAGTCA     180

CAGATCCGAC AACTGGGCAA AGCCTGGATG ATAGCCGCTT TCAGATACAG CAAACCGAAA     240

ATATCATTCG CAGCAAAACT CCCACGGGGC CGGAGCTAGA CACCAGCTAC AAAGGCTACA     300

TGAAACTGCT GGGCGAATGC AGTAGCAGTA TAGACTCCGT GAAGAGACTG GAGCACAAAC     360

TGAAGGAGGA AGAGGAGAGC CTTCCTGGCT TTGTTAACCT GCATAGTACC GAAACCCAAA     420

CGGCTGGTGT GATTGACCGA TGGGAGCTTC TCCAGGCCCA GGCATTGAGC AAGGAGTTGA     480

GGATGAAGCA GAACCTCCAG AAGTGGCAGC AGTTTAACTC AGACTTGAAC AGCATCTGGG     540

CCTGGCTGGG GGACACGGAG GAGGAGTTGG AACAGCTCCA GCGTCTGGAA CTCAGCACTG     600

ACATCCAGAC CATCGAGCTC CAGATCAAAA AGCTCAAGGA GCTCCAGAAA GCTGTGGACC     660

ACCGCAAAGC CATCATCCTC TCCATCAATC TCTGCAGCCC TGAGTTCACC CAGGCTGACA     720

GCAAGGAGAG CCGGGACCTG CAGGATCGCT TGTSGCAGAT GAATGGGCGC TGGGACCGAG     780

TGTGCTCTCT GCTGGAGGAG TGGCGGGGCC TGCTGCAGGA TGCCCTGATG CAGTGCCAGG     840

GTTTCCATGA AATGAGCCAT GGTTTGCTTC TTATGCTGGA GAACATTGAC AGAAGGAAAA     900

ATGAAATTGT CCCTATTGAT TCTAACCTTG ATGCAGAGAT ACTTCAGGAC CATCACAAAC     960

AGCTTATGCA AATAAAGCAT GAGCTGTTGG AATCCCAACT CAGAGTAGCC TCTTTGCAAG    1020

ACATGTCTTG CCAACTACTG GTGAATGCTG AAGGAACAGA CTGTTTAGAA GCCAAAGAAA    1080

AAGTCCATGT TATTGGAAAT CGGCTCAAAC TTCTCTTGAA GGAGGTCAGT CGTCATATCA    1140

AGGAACTGGA GAAGTTATTA GACGTGTCAA GTAGTCAGCA GGATTTGTCT TCCTGGTCTT    1200

CTGCTGATGA ACTGGACACC TCAGGGTCTG TGAGTCCCAY ATCAGGAAGG AGCACCCCAA    1260

ACAGACAGAA AACGCCACGA GGCAAGTGTA GTCTCTCACA GCCTGGACCC TCTGTCAGCA    1320

GTCCACATAG CAGGTCCACA AAAGGTGGCT CCGATTCCTC CCTTTCTGAG CCARGGCCAG    1380

GTCGGTCCGG CCGCGGCTTC CTGTTCAGAG TCCTCCGAGC AGCTCTTCCC CTTCAGCTTC    1440

TCCTGCTCCT CCTCATCGGG CTTGCCTGCC TTGTACCAAT GTCAGAGGAA GACTACAGCT    1500

GTGCCCTCTC CAACAACTTT GCCCGGTCAT TCCACCCCAT GCTCAGATAC ACGAATGGCC    1560

CTCCTCCACT CTGAACTAAG CAGATGCCAT CTGCAGAAGT GCTGGTAGCA TAAGGAGGAT    1620
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427

CGGGTCATAA GCAATCCCAA ACTACCAACA AGAGGACCTT GATCTTGGCG AAAGCCMTCG   1680

GTGTGGCAGC TTTAGCCTCC TCCAGATCAC ATGTGTGCAA ATTATGGCTT CAGAGGTGGA   1740

AGATAAACAG TGACGGGGGA ACAAACAGAC AACAAGAAGG TTTGGAAGAA ATCTGGTTTG   1800

AGACTCTGAA CCTTAGCACT AAGGAGATTG AGTAAGGACC TCCAAAGTTC CCCGGACTCA   1860

TGAATTCTGG GCCCTTGGCC NATTCTGTGC ACAGCCAAGG ACTTCAGTAG ACCATCTGGG   1920

CAGCTTTCCC ATGGTGCTGC TCCAACCATC AGATAAATGA CCCTCCCAAG CACCATGTCA   1980

GTGTCGTACA ATCTACCAAC CAACCAGTGC TGAAGAGATT TTAGAACCTT GTAACATACA   2040

ATTTTTAAGA GCTTATATGG CAGCTTCCTT TTTACCTTGT TTTCCTTTGG GGCATGATGT   2100

TTTAACCTTT GCTTTAGAAG CACAAGCTGT AAATCTAAAA GGCACTTTTT TTTAGAGGTA   2160

TAAAGAAAAA CTAGATGTAA TAAATAAGAT CATGGAAGGC TTTATGTGAA AAAAGTTGAA   2220

TGTTATAGTA AAAAAAAAAG ATATTTATGT ATGTACAGTT TGCTAAAGCC AAGTTTTGTT   2280

TGTATTGATT TCTTTGCATT TATTATAGAT ATTATAAAAT AAAAAAAAAA AAAAAAAAAC   2340

TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGTGAG   2379

(2) INFORMATION FOR SEQ ID NO: 176:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1348 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

GCGCCTTCAC GATGCCGGCG GTCAGTGGTC CAGGTCCCTT ATTCTGCCTT CTCCTCCTGC   60

TCCTGGACCC CCACAGCCCT GAGACGGGGT GTCCTCCTCT ACGCAGGTTT GAGTACAAGC   120

TCAGCTTCAA AGGCCCAAGG CTGGCATTGC CTGGGGCTGG AATACCCTTC TGGAGCCATC   180

ATGGAGGTGA GGGGCAGGGG TGGGGACCGC TATGCCCAGG GTCCCTCAAA GTGCTGGAGG   240

GGCTGTRACT TGGTGGGGAG TGGGTCTGTC ACAGCCATCC TCTGTCCAGG GTGGGGCAAG   300

GCCTGGGACA GTGCCAGGCA CCCCAGGACC CCTTCCAGGC TTGTCTCCTG CTCCACCGCC   360

TCAACACCCC CCACCCCTGC CCAAGCTGTT TCTCCTCTGC CTCTCTNNTT CCCTGCCCCA   420

GGACTTCTCT CTTCTCCTCT GCCTCTCCTT GGACCCCTGC CCTTCCTCTA CCTCTGACCT   480

GTGAACACAC AGACACATGC TCACACACTA AGTCCCARGC ACACMSAAAG GCAATGTGGA   540

CCAGCACAAA CCTCCACTCT CCCGGCTCCA TCCCARCGGG CCTGTGGCTG GCCATGAAAA   600

```
CTGGGGGCTA CCTGGAGGGA AGCATCCTCA TCCCAGGTGA GTGGGCACCA GCCCTTCCCT          660

GTATGTGTGT TGTGGGTGGA AGCAGGCATG AGAGCATCTT AGCCCATAGG TTTGTATTCA          720

GGGACTTCCA AACCCAGACC TACAAAGAGT GTGTCTTCTA CCAGATCTTG TTCAAAAAAG          780

GGTTTGTGAT GATGGAACTA CACGATAGAG GGAGTGAGCA AGAACAATGA GGATTAGAGT          840

GGAGCGTGAA ATAGTCTAGG AGCATGGCTT CCAAAACATA TGCTGTGAGG TCTGTCCACC          900

TGAGAGTTGG GCCATGGATT TAATTCTGAG CCTCTTAGCA GGCAAAGCAA AGACAGAAAG          960

CAGATCGGCT GTGGATTTCT GTCTATAAAA TGTGAGTTCT TGGCCGGGTG CGGTGGCTCA         1020

CGCCTGTAAT CCCGGCGCTT TGGGAGGCCA GGGCGGATGG GTCGCGAGGT CAGGAGGTTG         1080

GAAACCATCC TGGCCGGAAT GGTGAAGCCC TGACTCTACT AGAAGTGCAA AGATTGGCTG         1140

GGTGTGGTGG CGTGCGCCTG TGGTCCCAGC TTCTCGGGAG GCTGAGGCGG GAGAGTTGCT         1200

TGGGCCTGGG AGGCCGAGGT TGCGGTGAGC TGAGATCCTG CCATTGCACT TCAGCCTGGG         1260

CACAGAGCCA GACTCTGGCT CAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGCCCGTACC         1320

CAATTCGCCG NATATGATCG TAAACAAT                                            1348
```

(2) INFORMATION FOR SEQ ID NO: 177:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1502 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
CTCAAAATAA ATAAATAAAT AAAAATTTGT ATTCCATTGA TTTGGGTAGA CACCAGGAAT           60

GTGCATTTCT AACAAGCTTT CCAGGCGATC CTATAGTAAG TCATCTGTGG ACTACTTTAA          120

GAAACTCTTC TATAGAGAAT GGAGTTGGAT TAATAATAGG TGATTTTTTA CACTGGACTG          180

ATTCACAAGA ACCTAAACAG TAGTCCATGA AGCTGCTCAT CTGTGGTAAC TATTTGGCCC          240

CGTCTCACTC TGAAAGCAGC AGGAGATGTT GTTTACTTTG TTTCTATCCC CTTTGTCTGG          300

AGATTAATTT TGGAATGAAA GTTTTTCTCT CTATGCCATT CCTGGTTCTT TTCCAAAGCC          360

TCATACAAGA GGATTAGGTC ACAATGCATG CATTACCTTT TAAAAGAATG CGATATTGAT          420

ACCGATGCTT ACTTTTTTTT TTTTTNACTA CTTGTTTTAT TCCTTCCAGN AAAGTATAGC          480

CCGCCTTTCT ATAGCATAGT TCTCTTTAGG TGGAATGATT CCTATAAGAT TTCTCATTAT          540

TAAATCATGC ATTTTTCAAG ATGGAATCAA TMTTTGATTT AATCTAAGCT GATATTCTCA          600

TTTGTTAGAA GAACAACCTA CATGCTAGAG AGAGAGGAGG AAATATACCC ACGACCACAC          660
```

AGCCAGTTAG TATCCAGTTG GTGCTGGACT CCAGCCAGGT GTCCTGCCTC ATGGTAGTTA   720

AATGATATAT AGAAAAGGTA AATTTTTAAA GAAATATTTA TTAATATATT CCTATAAAAC   780

ATTTTAAAGG TAACCACATA AAAATGGTTA ATTTTTCCAT TCCAAAGTAA ATGCTAAGCA   840

TGTTTATTAA TGAAGCAGTA CTTCTGATTA GTATATGACA TTCTGAAGTT AATTAAACTC   900

ATTGCACTAA ATGTGTCTTC CTTGGTATAG TGGAGGATTT GAGGATTGGA ATATAGAGTA   960

GAGTGCTTGC TTAAGCCTGG GAGCCCATCT TTATAGCTAT TTGATGTAAG AAAAGAGACA   1020

TGGNCCATTT CTAAACTATA TAAGGTGAGT GTGTCTATTC CCAGCAGATA TAAAGGAAAA   1080

AGGAAACTTT TTTGATTCCC ACCTTCCCAG CCTCACCTAG CCATCTTCCA GCCTCAAATA   1140

TAGAGATGTT AGTGCAAGGT CCTGGGCTCT AGGTGATCAT TTCATAAGTC CTTTACAGAT   1200

AAAGAAAAAG TAGTGTTTGT ATGTTTGTTT TTAAGTAACC CCAAAACAAA TTTATATTGT   1260

ATTCAGCAAA ATTGGAATTC AGGTGTTTAA TTTTAGAACA TGAAGTGCCT GCTGTTTTAA   1320

GCATTGACTT GTATAAAAAG AATTGCATGT CTCCAGTAAG CTTATGGGTT TTCTCATTTT   1380

TAGGTATATG GCTTTTAATC ATGTAAAGTG AAACATTAGT TTTCTTGCAT TTTATTACAG   1440

GTTCTTTGTT GCAATAAAGA TGCTGCTGAA ATTAATTGAA AAAAAAAAAA AAAAAAACTC   1500

GA   1502

(2) INFORMATION FOR SEQ ID NO: 178:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1637 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

ATTTTCTAGC CCACAAGGAC TGAAGTTCAG ATCCAAAAGT TCACTTGCTA ATTATCTTCA   60

CAAAAATGGA GAGACTTCTC TTAAGCCAGA AGATTTTGAT TTTACTGTAC TTTCTAAAAG   120

GGGTATCAAG TCAAGATATA AAGACTGCAG CATGGCAGCC CTGACATCCC ATCTACAAAA   180

CCAAAGTAAC AATTCAAACT GGAACCTCAG GACCCGAAGC AAGTGCAAAA AGGATGTGTT   240

TATGCCGCCA AGTAGTAGTT CAGAGTTGCA GGAGAGCAGA GGACTCTCTA ACTTTACTTC   300

CACTCATTTG CTTTTGAAAG AAGATGAGGG TGTTGATGAT GTTAACTTCA GAAAGGTTAG   360

AAAGCCCAAA GGAAAGGTGA CTATTTTGAA AGGAATCCCA ATTAAGAAAA CTAAAAAAGG   420

ATGTAGGAAG AGCTGTTCAG GTTTTGTTCM AAGTGATAGC AAAAGAGAAT CTGTGTGTAA   480

430

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TAAAGCAGAT GCTGAAAGTG AACCTGTTGC ACAAAAAAGT CAGCTTGATA GAACTGTCTG        540

CATTTCTGAT GCTGGAGCAT GTGGTGAGAC CCTCAGTGTG ACCAGTGAAG AAAACAGCCT        600

TGTAAAAAAA AAAGAAAGAT CATTGAGTTC AGGATCAAAT TTTTGTTCTG AACAAAAAAC        660

TTCTGGCATC ATAAACAAAT TTTGTTCAGC CAAAGACTCA GAACACAACG AGAAGTATGA        720

GGATACCTTT TTAGAATCTG AAGAAATCGG AACAAAGTA GAAGTTGTGG AAAGGAAAGA        780

ACATTTGCAT ACTGACATTT TAAAACGTGG CTCTGAAATG GACAACAACT GCTCACCAAC        840

CAGGAAAGAC TTCACTGAAG ATACCATCCC ACGGAACACA GATAGAAAGA AGGAAAACAA        900

GCCTGTATTT TTCCAGCAAA TATAACAAAG AAGCTCTTAG CCCCCCACGA CGTAAAGCCT        960

TTAAGAAATG GACACCTCCT CGGTCACCTT TTAATCTCGT TCAAGAAACA CTTTTTCATG        1020

ATCCATGGAA GCTTCTCATC GCTACTATAT TTCTCAATCG GACCTCAGGC AAAATGGCAA        1080

TACCTGTGCT TTGGAAGTTT CTGGAGAAGT ATCCTTCAGC TGAGGTAGCA AGAACCGCAG        1140

ACTGGAGAGA TGTGTCAGAA CTTCTTAAAC CTCTTGGTCT CTACGATCTT CGGGCAAAAA        1200

CCATTGTCAA GTTCTCAGAT GAATACCTGA CAAAGCAGTG GAAGTATCCA ATTGAGCTTC        1260

ATGGGATTGG TGCACCCTGA AGACCACAAA TTAAATAAAT ATCATGACTG GCTTTGGGAA        1320

AATCATGAAA AATTAAGTCT ATCTTAAACT CTGCAGCTTT CAAGCTCATC TGTTATGCAT        1380

AGCTTTGCAC TTCAAAAAAG CTTAATTAAG TACAACCAAC CACCTTTCCA GCCATAGAGA        1440

TTTTAATTAG CCCAACTAGA AGCCTAGTGT GTGTGCTTTC TTAATGTGTG TGCCAATGGT        1500

GGATCTTTGC TACTGAATGT GTTTGAACAT GTTTTGAGAT TTTTTTAAAA TAAATTATTA        1560

TTTGACAACA ATCCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA        1620

AAAAAAAAAA AAAAAAA                                                       1637
```

(2) INFORMATION FOR SEQ ID NO: 179:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2911 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```
GGTGGTTTTT GTTCTGCAAT AGGCGGCTTA GAGGGAGGGG CTTTTTCGCC TATACCTACT        60

GTAGCTTCTC CACGTATGGA CCCTAAAGGC TACTGCTGCT ACTACGGGGC TAGACAGTTA        120

CTGTCTCAGC TCTAGGATGT GCGTTCTTCC ACTAGAAGCT CTTCTGAGGG AGGTAATTAA        180

AAAACAGTGG AATGGAAAAA CAGTGCTGTA GTCATCCTGT AATATGCTCC TTGTCAACAA        240
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431

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     TGTATACATT CCTGCTAGGT GCCATATTCA TTGCTTTAAG CTCAAGTCGC ATCTTACTAG        300

     TGAAGTATTC TGCCAATGAA GAAAACAAGT ATGATTATCT TCCAACTACT GTGAATGTGT        360
 5
     GCTCAGAACT GGTGAAGCTA GTTTTCTGTG TGCTTGTGTC ATTCTGTGTT ATAAAGAAAG        420

     ATCATCAAAG TAGAAATTTG AAATATGCTT CCTGGAAGGA ATTCTCTGAT TTCATGAAGT        480
10
     GGTCCATTCC TGCCTTTCTT TATTTCCTGG ATAACTTGAT TGTCTTCTAT GTCCTGTCCT        540

     ATCTTCAACC AGCCATGGCT GTTATCTTCT CAAATTTTAG CATTATAACA ACAGCTCTTC        600

     TATTCAGGAT AGTGCTGAAG ANGCGTCTAA ACTGGATCCA GTGGGCTTCC CTCCTGACTT        660
15
     TATTTTTGTC TATTGTGGCC TTGACTGCCG GGACTAAAAC TTTACAGCAC AACTTGGCAG        720

     GACGTGGATT TCATCACGAT GCCTTTTTCA GCCCTTCCAA TTCCTGCCTT CTTTTCAGAA        780
20
     ATGAGTGTCC CAGAAAAGAC AATTGTACAG CAAAGGAATG GACTTTTCCT GAAGCTAAAT        840

     GGAACACCAC AGCCAGAGTT TTCAGTCACA TCCGTCTTGG CATGGGCCAT GTTCTTATTA        900

     TAGTCCAGTG TTTTATTTCT TCAATGGCTA ATATCTATAA TGAAAAGATA CTGAAGGAAG        960
25
     GGAACCAGCT CACTGAARGC ATCTTCATAC AGAACAGCAA ACTCTATTTC TTTGGCATTC       1020

     TGTTTAATGG GCTGACTCTG GGCCTTCAGA GGAGTAACCG TGATCAGATT AAGAACTGTG       1080
30
     GATTTTTTTA TGGCCACAGT GCATTTTCAG TAGCCCTTAT TTTTGTAACT GCATTCCAGG       1140

     GCCTTTCAGT GGCTTTCATT CTGAAGTTCC TGGATAACAT GTTCCATGTC TTGATGGCCC       1200

     AGGTTACCAC TGTCATTATC ACAACAGTGT CTGTCCTGGT CTTTGACTTC AGGCCCTCCC       1260
35
     TGGAATTTTT CTTGGAAGCC CCATCAGTCC TTCTCTCTAT ATTTATTTAT AATGCCAGCA       1320

     AGCCTCAAGT TCCGGAATAC GCACCTAGGC AAGAAAGGAT CCGAGATCTA AGTGGCAATC       1380
40
     TTTGGGAGCG TTCCAGTGGG GATGGAGAAG AACTAGAAAG ACTTACCAAA CCCAAGAGTG       1440

     ATGAGTCAGA TGAAGATACT TTCTAACTGG TACCCACATA GTTTGCAGCT CTCTTGAACC       1500

     TTATTTTCAC ATTTTCAGTG TTTGTAATAT TTATCTTTTC ACTTTGATAA ACCAGAAATG       1560
45
     TTTCTAAATC CTAATATTCT TTGCATATAT CTAGCTACTC CCTAAATGGT TCCATCCAAG       1620

     GCTTAGAGTA CCCAAAGGCT AAGAAATTCT AAAGAACTGA TACAGGAGTA ACAATATGAA       1680
50
     GAATTCATTA ATATCTCAGT ACTTGATAAA TCAGAAAGTT ATATGTGCAG ATTATTTTCC       1740

     TTGGCCTTCA AGCTTCCAAA AAACTTGTAA TAATCATGTT AGCTATAGCT TGTATATACA       1800

     CATAGAGATC AATTTGCCAA ATATTCACAA TCATGTAGTT CTAGTTTACA TGCCAAAGTC       1860
55
     TTCCCTTTTT AACATTATAA AAGCTAGGTT GTCTCTTGAA TTTTGAGGCC CTAGAGATAG       1920

     TCATTTTGCA AGTAAAGAGC AACGGGACCC TTTCTAAAAA CGTTGGTTGA AGGACCTAAA       1980
60
     TACCTGGCCA TACCATAGAT TTGGGATGAT GTAGTCTGTG CTAAATATTT TGCTGAAGAA       2040
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    GCAGTTTCTC AGACACAACA TCTCAGAATT TTAATTTTTA GAAATTCATG GGAAATTGGA          2100

    TTTTTGTAAT AATCTTTTGA TGTTTTAAAC ATTGGTTCCC TAGTCACCAT AGTTACCACT          2160

5   TGTATTTTAA GTCATTTAAA CAAGCCACGG TGGGGCTTTT TTCTCCTCAG TTTGAGGAGA          2220

    AAAATCTTGA TGTCATTACT CCTGAATTAT TACATTTTGG AGAATAAGAG GGCATTTTAT          2280

10  TTTATTAGTT ACTAATTCAA GCTGTGACTA TTGTATATCT TTCCAAGAGT TGAAATGCTG          2340

    GCTTCAGAAT CATACCAGAT TGTCAGTGAA GCTGATGCCT AGGAACTTTT AAAGGGATCC          2400

    TTTCAAAAGG ATCACTTAGC AAACACATGT TGACTTTTAA CTGATGTATG AATATTAATA          2460

15  CTCTAAAAAT AGAAAGACCA GTAATATATA AGTCACTTTA CAGTGCTACT TCACACTTAA          2520

    AAGTGCATGG TATTTTTCAT GGTATTTTGC ATGCAGCCAG TTAACTCTCG TAGATAGAGA          2580

20  AGTCAGGTGA TAGATGATAT TAAAAATTAG CAAACAAAAG TGACTTGCTC AGGGTCATGC          2640

    AGCTGGGTGA TGATAGAAGA GTGGGCTTTA ACTGGCAGGC CTGTATGTTT ACAGACTACC          2700

    ATACTGTAAA TATGAGCTTT ATGGTGTCAT TCTCAGAAAC TTATACATTT CTGCTCTCCT          2760

25  TTCTCCTAAG TTTCATGCAG ATGAATATAA GGTAATATAC TATTATATAA TTCATTTGTG          2820

    ATATCCACAA TAATATGACT GGCAAGAATT GGTGGAAATT TGTAATTAAA ATAATTATTA          2880

30  AACCTAAAAA AAAAAAAAAA AAAAACTCGA G                                          2911



35  (2) INFORMATION FOR SEQ ID NO: 180:

         (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 519 base pairs
                 (B) TYPE: nucleic acid
40               (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

45  GGCACGAGCC CCAGGCCAGC CAGGGCCAGG CCTACTTTGG CCACCCTTAA ATTAGAATGT           60

    GGGGTCAGGG GTCACAGAAA AGCCATTTCT CTGACCTAGT GTTTGGCGTC CGGGAACTCT          120

    GTGCCCAACC TTCAGACCCT GGCAGTCCTC ACTGAGGCCA TTGGCCCAGA GCCCGCCATC          180

50  CCCCGARACC CCCGGGAGCC GCCTGTTGCC ACGTCCACAC CTGCCACACC CTCTGCCGGG          240

    CCCCAGCCCC TCCCAACCGG GACCGTGCTG GTCCCTGGGG GTCCTGCCCC ACCTTGCCTT          300

55  GGGGAGGCAT GGGCCCTCCT CCTCCCACCC TGCCGGCCGT CACTCACCTC TTGCTTCTGG          360

    TCCCCCAGGC CTAGCCCTTG GAAGGAGACA GGAGTCTAGG GAGGCTGAAG CCCACTCCCG          420

    GGGAGGCCCG TGCTCCTCCA GCCCCAGGGA CAGCAAGGAA AAGAGAAGAG AGCAGAGCAT          480
60
```

TTCATGGCTC TAATAAAAAA AAAAAAAAAA AAAACTCGA   519

(2) INFORMATION FOR SEQ ID NO: 181:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 968 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

TCCCCTTGGG GCCGGAAAAA GCGGGGTTGG CCTGNCCATT GGTTNTCCAT GCCGCCCGCC   60

CATGCCCCAG TACTAGCCTG CAGTCCCAAT GTAGCCCCTC CCTCYTCCMA GAGCCCYTCM   120

AACCGCCCCG STCANTTGTG ATTTCAGGAG GATTTGATGA AGATGTTAAA GCGAAAGTGG   180

AGAACCTTCT CGGGATTTCC AGCCTGGAAA AAACGGACCC TGTTAGGCAA GCACCCTGCA   240

GCCCTCCCTG TCCCCTTCTT CCCCTCCCCT TCYCCCGCCC GTGGAGACAG CTGTTYTCAG   300

CAGGGCTCTC CGCAGGGAGG GGGCCGGCTC CTTCCCTGGC AGCAACATCC TTGCCCTTGT   360

CACACAAGTC AGCCTCCATC TGCGCAGCTC TGTGGATGCG CTGCTGGAGG GCAACAGGTA   420

TGTCACTGGC TGGTTCAGCC CCTACCACCG CCAGCGGAAG CTCATCCACC CGGTCATGGT   480

TCAGCACATC CAGCCCGCAG CGCTCAGCCT CCTGGCACAG TGGAGCACCC TCGTGCAGGA   540

GCTGGAGGCT GCCCTGCAGC TGGCTTTCTA CCCGGATGCC GTGGAGGAGT GGCTGGAGGA   600

AAACGTGCAC CCCAGCCTGC AGCGGCTGCA ARCTCTGCTG CAGGACCTCA GCGAGGTGTC   660

TGCCCCCCCG CTGCCACCCA CCAGCCCTGG CAGGGACGTT GCTCAGGACC CCTGAGGGGA   720

GAGCTCATGC CAGGGGGCTC CTGCTGGAGG CTGGGGGGGC TCTGCWYTKY CWWWTGGCCT   780

GGGCAATACG GCCCACGTGG GCGTCGTGCC CTCTGGCCCA GCAGTGTCTT GCCCACACTC   840

AGTTCCTGAG GGCCCTGGGC AGCCCCTGGG GGAGAGACTA GAAAACACAG AAGGAAGCAG   900

CACAGGGAGA CCCGCTTTGT GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGAGT   960

GGAAGCTG   968

(2) INFORMATION FOR SEQ ID NO: 182:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1128 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

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TGTAAAAGTT ATCAGTAATC CTAATTCTTT TCCTGGGTTT TCCTTTTGTC ACTTATTAAT      60

CAGTTTTTGA AAGGACGAAT GAATTTAGAG ATGTACTCTG GAGCAGTATC ATGTTAAACC     120

AGGGGTATAT TAGAAAAATC ATCCTCATAA TCATTCTGGG AAGTTTTTCC TCCCCAAAAA     180

AAGCCATCCT GATGGGTTTT CAAAACCAGA AAAAAGCTCT TAATGAGGAA CAGACCACTG     240

GAGTACCCAT GAGCATCTCA GGAAAACTGA GACCCTCGAG AAGCCTTGAT TTCGTGCAAC     300

CCCCAAGGTT TCAGAGCCAG CAGCCCAGTG CTGTGGTTGA CAGACGTGGT TTTKTGGRGA     360

AAGCAGCCAG AGGCCAGGAA TTTTCAGAGT CGTGAGTCAC GRTYTCCCAC CCAAGATTAG     420

AGCAMAGATT AGCCATACTG AGATTTGGTA AAATCATTCT GTCTAAGCAA TGGAGGTGTG     480

TGCAMACGTG CAGTGCCTGT TCACAGGGGA TGCAGGCAGA TCSYGGGTTT AGGATGGGGR     540

AGGCCACCGC ACCCCCYTTC AYTGCTCTGC ACCTGCTCCC TCACGTGGAC ACTGTCCACA     600

ACTGTGGCTC TCACAGGACA GTTGCCCAAG GAGCTCATAT CTTATTGGAG ATAGGGGGTC     660

GTACAGGTGA CATTCATGAG CAGTGTGAGC CGGGTGACAT GGGGGTGTCA ACCCAGCATC     720

TGTCCAGGAG CTCCTCCTGC AGCGGCTCTG GCAGGTGGCC TGAGGCTCCT TTTTGAGAGA     780

GAACTGTTTG GCCTTCCTGT CTCCTCTCCT CTGATCTGTT CTTTCTTGGA ACACCACCCA     840

AGAACGTCAC CTCCTCCATC AGATTGTGAG CTCCTGGAGG GCAGGAGCTG TGTCCTTCTA     900

TTCATCTTCC TATCCCCAGA ACCTTGCACA GATCCTGGAA TGTGGTAGGT GCTCAGTAAA     960

TGTGTGTTGA ATAAATGAAT GAATGAATGA ACAAATGAAT GAATTTGCTT ACTTCAAGGC    1020

AAAAGAACCA TGAAACTGTA TTTRGAGTTT CTATGTTATA GCAGTCAGCA AATCCTATTA    1080

AATACTTTGT GTTTCCAAGC AAAAAAAAAA AAAAAAAAAA AAACTCGA               1128
```

(2) INFORMATION FOR SEQ ID NO: 183:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2276 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
CCGCGGCGTC TGACCTCATG GCGTAGAGCC TAGCAACAGC GCAGGCTCCC AGCCGAGTCC      60

GTTATGGCCG CTGCCGTCCC GAAGAGGATG AGGGGGCCAG CACAAGCGAA ACTGCTGCCC     120

GGGTCGGCCA TCCAAGCCCT TGTGGGGTTG GCGCGGCCGC TGGTCTTGGC GCTCCTGCTT     180

GTGTCCGCCG CTCTATCCAG TGTTGTATCA CGGACTGATT CACCGAGCCC AACCGTACTC     240
```

```
        AACTCACATA TTTCTACCCC AAATGTGAAT GCTTTAACAC ATGAAAACCA AACCAAACCT      300

  5     TCTATTTCCC AAATCAGCAC CACCCTCCCT CCCACGACGA GTACCAAGAA AAGTGGAGGA      360

        GCATCTGTGG TCCCTCATCC CTCGCCTACT CCTCTGTCTC AAGAGGAAGC TGATAACAAT      420

        GAAGATCCTA GTATAGAGGA GGAGGATCTT CTCATGCTGA ACAGTTCTCC ATCCACAGCC      480

 10     AAAGACACTC TAGACAATGG CGATTATGGA GAACCAGACT ATGACTGGAC CACGGGCCCC      540

        AGGGACGACG ACGAGTCTGA TGACACCTTG GAAGAAAACA GGGGTTACAT GGAAATTGAA      600

        CAGTCAGTGA AATCTTTTAA GATGCCATCC TCAAATATAG AAGAGGAAGA CAGCCATTTC      660

 15     TTTTTTCATC TTATTATTTT TGCTTTTTGC ATTGCTGTTG TTTACATTAC ATATCACAAC      720

        AAAAGGAAGA TTTTTCTTCT GGTTCAAAGC AGGAAATGGC GTGATGGCCT TTGTTCCAAA      780

 20     ACAGTGGAAT ACCATCGCCT AGATCAGAAT GTTAATGAGG CAATGCCTTC TTTGAAGATT      840

        ACCAATGATT ATATTTTTTA AAGCACTGTG ATTTGAATTT GCTTATGTAA TTTTATTTGC      900

        TTGACTTTTT ATATGATATT GTGCAAATGT TTGCCATAGG CAATTGGTAC TTAAATGAGA      960

 25     GGTGAGTCTC TCTTTTGCCT TGGTGCTTTG GAAATTAAAT GTCACAAACG AGTATATAAT     1020

        TTTTTATCTG TACTTTTAGA GCTGAGTTTA ATCAGGTGTC CAAAATGTGA GTTAAACATT     1080

        ACCTTATATT TACACTGTTA GTTTTTATTG TTTTAGATTT ATTATGCTTC TTCTGGAAGT     1140

 30     ATTAGTGATG CTACTTTTAA AAGATCCCAA ACTTGTAACT AAATTCTGAC ATATCTGTTA     1200

        CTGCTGACTC ACATTCATTC TCCGCCATTC AAATACTATT TTTTATCCAC ATTTTTTTTT     1260

 35     GTTCCCAAAC TGTAATGTAC AAGGATATGT GTGATAATGC TTTGGATTTG AGTAATATTT     1320

        TTTTTTCTTC CAAGAAAACT GCTTTGGATA TTTTTAGATA ATTTAAACAT AATTTAGGAT     1380

 40     AATGATATTG CTCAATCTGA CCACAATTTT AGGTAAAACA TTAAATGTGT CAGAAATCTT     1440

        GGCAACAGAG ACTCTGCAGC TTGCAGTGGA CATAGATAAA ATGTTACAGA GATACTATTT     1500

        TTTTGGTTGG AATTACTATA TTAAATTTAG AAGCAGAAAC TGGTAAAATG TTAAATACAT     1560

 45     GTACAATTGC TTTTAGTTAG CAATTGATTG TAGCATGGGT TCCTCCAAGG TTTCAAGCAA     1620

        TGGGCAGAGT TTAAAATTAT ATCAGATTCG TTTACTTCGT TTATTATTTT ACAGTAAATT     1680

 50     TGAATAAATC TTAGGGGTCA TTATCACTTA AATAATACTG TACCTAGGTC TTTCAAATTA     1740

        AAATTATACC TGAATGAAGT TGTTTGTATA CATAAAGGAT ATTTGTGTAC AATTACCTTT     1800

        TTTCCCCCAC ACTTGTTTTC TTTGTTTTTG TTTTTTATGG CAACTGGAAA GTATTTACTA     1860

 55     TGGGATTCAT TTATGTCTGT CTTTCTATCA TAAAGAATTG ATCAATATGT AAATATGTGA     1920

        TTTGAACCAT GGTTGACTTA CAAGTGTCAC TACAGCTTTT TAGAAAACAT AGCCCTAATA     1980

 60     TATGTTAAGC AGGACCCGGG TGAGCCAGTG GGCTTGCGCT TTATGTAGAG CTGGAAGAAG     2040
```

436

GCCGTCCATC CTGTCTCTTG GGCGGACAGT GTACTTTCCT AATAGGGAAG GGAAGCACAA   2100

TGGAAATACC CCTGAACCGT TTTATTGCAG TAATTTTTTT CATATCTGAA ACTATTATTT   2160

AATATTTTGA ATAAGATTTT AAAAAATAAA TGGCAAAGAT ATAAATCTAA AAAAAAAAAA   2220

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA   2276

(2) INFORMATION FOR SEQ ID NO: 184:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2500 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TCCAAGCTAC GCCACTCGGG CTGGGGCGTT GGGAGCGGGA GTGCAGAGCG TGGTCGTGGC   60

GGCGGCGGTG AGAAGAGCGA GGCGKAGGAG GGGGTGCCAT GGCCGGGCAG CAGTTCCAGT   120

ACGATGACAG TGGGAACACC TTCTTCTACT TCCTCACCTC CTTCGTGGGG CTCATCGTGA   180

TCCCGGCGAC ATACTACCTC TGGCCCCGAG ATCAGAATGC CGAGCAAATT CGATTAAAGA   240

ATATCAGAAA AGTATATGGA AGGTGTATGT GGTACGTTTA CGGTTATTAA AACCCCAGCC   300

AAATATTATT CCTACAGTAA AGAAAATAGT TCTGCTTGCA GGATGGGCAT TGTTCTTATT   360

CCTTGCATAT AAAGTTTCCA AAACAGACCG AGAATACCAA GAATACAATC CTTATGAAGT   420

ATTAAATTTG GATCCTGGAG CCACAGTAGC AGAAATTAAA AAACAATATC GTTTGCTGTC   480

ACTTAAATAT CATCCAGATA AAGGAGGTGA TGAGGTTATG TTCATGAGGA TAGCAAAAGC   540

TTATGCTGCT TTAACGGATG AAGAGTCCCG GAAAAATTGG GAAGAATTTG GAAATCCAGA   600

TGGGCCTCAA GCCACAAGCT TTGGAATTGC CCTGCCAGCT TGGATAGTTG ACCAGAAAAA   660

TTCAATTCTG GTTTTACTTG TATATGGATT GGCATTTATG GTTATCCTTC CAGTTGTTGT   720

GGGCTCTTGG TGGTATCGCT CAATACGCTA TAGTGGAGAC CAGATTCTAA TACGSACAAC   780

ACAGATTTAT ACATACTTTG TTTATAAAAC CCGAAATATG GATATGAAAC GTCTTATCAT   840

GGTTTTGGST GGAGCTTCTG AATTTGATCC TCAGTATAAT AAAGATGCCA CAAGCAGACC   900

AACGGATAAT ATTCTAATAC CACAGCTAAT CAGAGAAATT GGCAGCATTA ATTTAAAGAA   960

GAATGAGCCT CCACTTACCT GCCCATATAG CCTGAAGGCC AGAGTTCTTT TACTGTCTCA   1020

TCTTGCTAGA ATGAAAATTC CTGAGACCCT TGAAGAAGAT CAGCAATTCA TGCTAAAAAA   1080

GTGTCCTGCC CTACTTCAAG AAATGGTTAA TGTAATCTGC CAACTAATAG TAATGGCCCG   1140

```
GAACCGTGAA GAAAGGGAGT TTCGTGCTCC AACTTTGGCA TCCCTAGAAA ACTGCATGAA      1200

GCTTTCTCAG ATGGCCGTTC AGGGACTTCA GCAATTTAAG TCTCCCCTTC TGCAGCTCCC      1260

TCATATTGAA GAGGACAATC TTAGACGGGT TTCTAATCAT AAGAAGTATA AAATTAAAAC      1320

TATCCAGGAT TTGGTGAGTT TAAAAGAATC AGATCGTCAC ACTCTACTGC ACTTCCTTGA      1380

AGATGAAAAA TATGAAGAGG TTATGGCTGT CCTTGGGAGT TTTCCATATG TGACCATGGA     . 1440

TATAAAATCA CAGGTGTTAG ATGATGAAGA TAGCAACAAC ATCACAGTAG GATCCTTAGT      1500

TACAGTGTTG GTTAAGTTGA CAAGGCAAAC AATGGCTGAA GTATTTGAAA AGGAGCAGTC      1560

CATCTGTGCT GCAGAGGAAC AGCCAGCAGA AGATGGGCAG GGTGAAACTA ACAAGAACAG      1620

GACAAAAGGA GGATGGCAAC AGAAGAGTAA AGGACCCAAG AAAACTGCTA AATCAAAAAA      1680

AAAGAAACCT TTAAAAAAAA AACCTACACC TGTGCTATTA CCACAGTCAA AGCAACAGAA      1740

ACAAAAGCAG GCAAATGGAG TCGTTGGGAA TGAAGCTGCA GTAAAGGAAG ATGAAGAAGA      1800

AGTTTCAGAT AAGGGCAGTG ATTCTGAAGA AGAAGAAACC AATAGAGATT CCCAAAGTGA      1860

GAAAGATGAT GGTAGTGACA GAGACTCTGA TAGAGAGCAA GATGAAAAAC AAAACAAAGA      1920

TGATGAAGCA GAGTGGCAAG AATTACAACA AAGCATACAG CGAAAAGAGA GAGCTCTATT      1980

GGAAACCAAA TCAAAAATAA CACATCCTGT GTATAGCCTT TACTTTCCTG AGGAAAAACA      2040

AGAATGGTGG TGGCTTTACA TTGCAGATAG GAAGGAGCAG ACATTAATAT CCATGCCATA      2100

TCATGTGTGT ACGCTGAAAG ATACAGAGGA GGTAGAGCTG AAGTTTCCTG CACCAGGCAA      2160

GCCTGGAAAT TATCAGTATA CTGTGTTTCT GAGATCAGAC TCCTATATGG GTTTGGATCA      2220

GATTAAACCA TTGGAAGTTK GGAAGTTCAT GAGGCTGAAG CCTGTGCCAG AAAATCACCC      2280

ACAGTGGGAT ACAGCAATAG AGGGGGATGA AGACCAGGAG GACAGTGAGG GCTTTGAAGA      2340

TAGCTTTGAG GGAGGAAGAG GGAGGGAGGA AGGAAGGTGG TGGACTTAAG GCAGTTACTC      2400

TGGAATGGGA CCCACAGTGT TTTGCACCAT ATTTTGGCAA TTTTTTTTGC CCGTTTTTNG      2460

GAAGTGTTTT CCNTNAANCC CAGGAACCAT TACAGAACCG                            2500
```

(2) INFORMATION FOR SEQ ID NO: 185:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1337 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```
CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC          60
```

```
TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA      120

GCCAGCGTGG CGGGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG      180

GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTTG      240

CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT      300

CTTGGGCCTC CTGACCCTAG ACCACGGACA TTACCGCCGC TGCCACCGGG CCCTACCCCT      360

GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGC CGCGGGGCTC CGAGGGAGGC      420

AATGGCAGCA ACCCTGTGGC CGGGCTTGAG ACGGACGATC ACGGAGGGAA GGCCGGGGAA      480

GGCTCGGTGG GTGGCGGCCT TGCTGTGAGC CCCAACCCTG GCGACAAGCC CATGACCCAG      540

CGGGCCCTGA CCGTGTTGAT GGTGGTGAGC GGCGCGGTGC TGGTGTACTT CGTGGTCAGG      600

ACGGTCAGGA TGAGAAGAAG AAACCGAAAG ACTAGGAGAT ATGGAGTTTT GGACACTAAC      660

ATAGAAAATA TGGAATTGAC ACCTTTAGAA CAGGATGATG AGGATGATGA CAACACGTTG      720

TTTGATGCCA ATCATCCTCG AAGATAAGAA TGTGCCTTTT GATGAAAGAA CTTTATCTTT      780

CTACAATGAA GAGTGGAATT TCTATGTTTA AGGAATAAGA AGCCACTATA TCAATGTTGG      840

GGGGGTATTT AAGTTACATA TATTTTAACA ACCTTTAATT TGCTGTTGCA ATAAATACCG      900

TATCCTTTTA TTATATCTTT ATATGTATAG AAGTACTCTR TTAATGGGCT CAGAGATGTT      960

GGGGATAAAG TATACTGTAA TAATTTATCT GTTTGAAAAT TACTATAAAA CGGTGTTTTC     1020

TGATCGGTTT TTGTTTCCTG CTTACCATAT GATTGTAAAT TGTTTTATGT ATTAATCAGT     1080

TAATGCTAAT TATTTTTGCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAACCAAC     1140

TGGTGTGTAA AAATAATTTA AAATTTCCTT TACTGAAAGG TATTTCCCAT TTTTGTGGGG     1200

AAAAGAAGCC AAATTTATTA CTTTGTGTTG GGGTTTTTAA AATATTAAGA AATGTCTAAG     1260

TTATTGTTTG CAAAACAATA AATATGATTT TAAATTCTCT TAAAAAAAAA AAAAAAAACC     1320

CCGGGGGGGG GCCCGGN                                                    1337
```

(2) INFORMATION FOR SEQ ID NO: 186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 941 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
GGCACGAGCC TGGACGCAGC AGCCACCGCC GCGTCCCTCT CTCCACGAGG CTGCCGGCTT       60
```

439

```
AGGACCCCCA GCTCCGACAT GTCGCCCTCT GGTCGCCTGT GTCTTCTCAC CATCGTTGGC    120

CTGATTCTCC CCACCAGAGG ACAGACGTTG AAAGATACCA CGTCCAGTTC TTCAGCAGAC    180

TCAACTATCA TGGACATTCA GGTCCCGACA CGAGCCCCAG ATGCAGTCTA CACAGAACTC    240

CAGCCCACCT CTCCAACCCC AACCTGGCCT GCTGATGAAA CACCACAACC CCAGACCCAG    300

ACCCAGCAAC TGGAAGGAAC GGATGGGCCT CTAGTGACAG ATCCAGAGAC ACACAAGAGC    360

ACCAAAGCAG CTCATCCCAC TGATGACACC ACGACGCTCT CTGAGAGACC ATCCCCAAGC    420

ACAGACGTCC AGACAGACCC CCAGACCCTC AAGCCATCTG GTTTTCATGA GGATGACCCC    480

TTCTTCTATG ATGAACACAC CCTCCGGAAA CGGGGGCTGT TGGTCGCAGC TGTGCTGTTC    540

ATCACAGGCA TCATCATCCT CACCAGTGGC AAGTGCAGGC AGCTGTCCCG GTTATGCCGG    600

AATCATTGCA GGTGAGTCCA TCAGAAACAG GAGCTGACAA CCYGCTGGGC ACCCGAAGAC    660

CAAGCCCCCT GCCAGCTCAC CGTGCCCAGC CTCCTGCATC CCCTCGAAGA GCCTGGCCAG    720

AGAGGGAAGA CACAGATGAT GAAGCTGGAG CCAGGGCTGC CGGTCCGAGT CTCCTACCTC    780

CCCCAACCCT GCCCGCCCCT GAAGGCTACC TGGCGCCTTG GGGGCTGTCC CTCAAGTTAT    840

CTCCTCTGYT AAGACAAAAA GTAAAGCACT GTGGTCTTTG CAAAAAAAAA AAAAAAAAAA    900

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACTCG A                        941
```

(2) INFORMATION FOR SEQ ID NO: 187:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 654 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
GAATTCGGCA CGAGGCAGCT TGTGCTTTAA AGGAGGTGTT CAAAGCATGT CTGAGCAGAG    60

ACTTTTGGGC TCTGTTTTAA TTAATACTTT AAAATAATTC ATATTTAAAA TATCARATGT    120

TTCCATAAAG AGGAGGATGT TTAAATGCCT CCAGACTACA TTCCTTTTTA TTSCTTGATT    180

TTACCTGGGA GTCCAAAGTT CAATTCCCAT AAAGCAAGCG TTTTATTTGT CACTTTCAAT    240

ATACATCCGA TTGCCATGCT TAAGATGCAA TATGGGCTGC GGAAATAGGT TAACCCACAG    300

GCTCCCAGGG CCCAGTGTAG AAGGTGAGAG ATTCGTGTAA AATGATTCAA ATAAAAGGAA    360

GACCCTGGCC GGGTGCCGTA RCTCACGCCT GTAATCCCAG CACTTTGGGA GGCCGAAGCG    420

AGTGGATGAC GAGGTTAGGA GTTGGAGACC AGCCTGGCCA ACATCGTGAA ACCCCGTCTC    480

TACTAAAAAT ACAAAAATTA GCCGGGCATG GTGGCAGGCA CCTGTAATCC TAGCTAGTTG    540
```

440

```
GGAGGCTGAG GCAGGAGAAT CGTTTGAATC TGGGAGTTGG AGGTTGTCAG TGAGCTGAGA          600

TCGCGCCACA GCACTCCAGC CTGGGTGACA GGGTGAGACT CTGTCTCAAA NAGA                654
```

(2) INFORMATION FOR SEQ ID NO: 188:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1848 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
GAAACTGGAC CGGAGAACCG GAGCGAAGCG AAGCGGAAGC CCGGAATGAG GCCGGACTGG          60

AAAGCCGGAG CGGGGCCAGG CGGGCCTCCC CAAAAGCCTG CCCCTTCATC CCAGCGGAAA          120

CCGCCGGCCC GGCCGAGCGC GGCGGCCGCT GCGATTGCAG TCGCGGCGGC GGAGGAAGAG          180

AGACGGCTCC GGCAGCGGAA CCGCCTGAGG CTGGAGGAGG ACAAACCGGC CGTGGAGCGG          240

TGCTTGGAGG AGCTGGTCTT CGGCGACGTC GAGAACGACG AGGACGCGTT GCTGCGGCGT          300

CTGCGAGGCC CGAGGGTTCA AGAACATGAA GACTCGGGTG ACTCAGAAGT GGAGAATGAA          360

GCAAAAGGTA ATTTTCCACC TCAAAAGAAG CCAGTTTGGG TGGATGAAGA AGATGAAGAT          420

GAGGAAATGG TTGACATGAT GAACAATCGG TTTCGGAAGG ATATGATGAA AAATGCTAGT          480

GAAAGTAAAC TTTCGAAAGA CAACCTTAAA AAGAGACTTA AGAAGAATT CCAACATGCC          540

ATGGGAGGAG TACCTGCCTG GGCAGAGACT ACTAAGCGGA AAACATCTTC AGATGATGAA          600

AGTGAAGAGG ATGAAGATGA TTTGTTGCAA AGGACTGGGA ATTTCATATC CACATCAACT          660

TCTCTTCCAA GAGGCATCTT GAAGATGAAG AACTGCCAGC ATGCGAATGC TGAACGTCCT          720

ACTGTTGCTC GGATCTCCAT CTGTGCAGTT CCATCCCGGT GCACAGATTG TGATGGTTGC          780

TGGGATTAGA TAATGCTGTA TCACTATTTC AGGTTGATGG GAAAACAAAT CCTAAAATTC          840

AGAGCATCTA TTTGGAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG          900

AAGTTTTAGC CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA          960

AGTTAATTCC TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG          1020

TCTCCCCAGA TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG          1080

CAATGAAGAC CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA          1140

CATTCTCTTC AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT          1200

GGGATGTGAA CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT          1260
```

441

TAAGCATTGC CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG   1320

TAAATATATA CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA   1380

TAATGAACTT GGTTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG   1440

CAATTGCTTC AGAAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG   1500

TATTTTCAAA CTTCCCAGTC ATTAAAAATA AGAATATTTC TCATGTTCAT ACCATGGATT   1560

TTTCTCCGAG AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA   1620

GGTTGCACCA TTACTCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG   1680

AAGCCTGTCT TGATATATCA TCTCAGAAAC TTTCCTGAAT ATGTGATAAT ATATGGAAAA   1740

TGATTTATAG ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT   1800

TTTGTTTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACTCGA   1848

(2) INFORMATION FOR SEQ ID NO: 189:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1146 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AAAAAAAACC CAGGGGAACN TTGGGGGCCG CTTTNNNTTC CCCCTCCAGG CCATTGGGGA   60

ATTCTTCAAG TTAATCCTGC TTTGCTCTTG GCCAACAGGG CTTGTAGGGG GGAGAGACCC   120

AGGATCATCA AGGGGTTCGA GTGCAAGCCT CACTCCCAGC CCTGGCAGGC AGCCCTGTTC   180

GAGAAGACGC GGCTACTCTG TGGGGCGACG CTCATCGCCC CCAGATGGCT CCTGACAGCA   240

GCCCACTGCC TCAAGCCCCG CTACATAGTT CACCTGGGGC AGCACAACCT CCAGAAGGAG   300

GAGGGCTGTG AGCAGACCCG GACAGCCACT GAGTCCTTCC CCCACCCCGG CTTCAACAAC   360

AGCCTCCCCA ACAAAGACCA CCGCAATGAC ATCATGCTGG TGAAGATGGC ATCGCCAGTC   420

TCCATCACCT GGGCTGTGCG ACCCCTCACC CTCTCCTCAC GCTGTGTCAC TGCTGGCACC   480

AGCTGYCTCA TTTCCGGCTG GGGCAGMACG TCCAGCCCCC AGTTACGCCT GCCTCACACC   540

TTGSGATGCG CCAACATCAC CATCATTGAG CACCAGAAGT GTGAGAACGC CTACCCCGGC   600

AACATCACAG ACACCATGGT GTGTGCCAGC GTGCAGGAAG GGGCAAGGA CTCCTGCCAG   660

GGTGACTCCG GGGCCCTCT GGTCTGTAAC CAGTCTCTTC AAGGCATTAT CTCCTGGGGC   720

CAGGATCCGT GTGCGATCAC CCGAAAGCCT GGTGTCTACA CGAAAGTCTG CAAATATGTG   780

GACTGGATCC AGGAGACGAT GAAGAACAAT TAGACTGGAC CCACCCACCA CAGCCCATCA   840

442

```
     CCCTCCATTT CCACTTGGTG TTTGGTTCCT GTTCACTCTG TTAATAAGAA ACCCTAAGCC     900

     AAGACCCTCT ACGAACATTC TTTGGGCCTC CTGGACTACA GGAGATGCTG TCACTTAATA     960
5
     ATCAACCTGG GGTTCGAAAT CAGTGAGACC TGGATTCAAA TTCTGCCTTG AAATATTGTG    1020

     ACTCTGGGAA TGACAACACC TGGTTTGTTC TCTGTTGTAT CCCCAGCCCC AAAGACAGCT    1080

10   CCTGGCCATA TATCAAGGTT TCAATAAATA TTTGCTAAAT GAAAAARAAA AAAAAAAAAA    1140

     ACTCGA                                                              1146
```

15

(2) INFORMATION FOR SEQ ID NO: 190:

         (i) SEQUENCE CHARACTERISTICS:
20   (A) LENGTH: 906 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```
     ACTCCCTCAC CCAGGTCCCA GCCCTGGGAA CCACCTACCG TGAGCCCTTT TGCAGATATA     60

     GACTCATTTC ATCCTCAGAT GGTCCTTCAA GGTAGGTACT TTAGTCCCAT TTTAGAGATG    120
30
     AGACGATTGA GGCCAGAGGG GTGNNGTAAC TTGCCTGGGG GCTCACGAGC ACAAAAGGAG    180

     CCGAGGCAGG ATCTGACCCT TGTTCTCTGG CCTCACTGCC CTCACTTTGC CATGACCCGA    240

35   AGTTATGTCC CTACAAAGCA ATGCATGGTC CAAGGYTCTT TTTATTGTAT TTTTATTTTT     300

     AAGGGTCCTG TTCAAAACTG GTGTGAGCTC TGAGGAGTCC TGAACCCTGG GTGCAGCATC    360

     CTAGCATCCT GGGAGTCCTT TTCTGCCCAC ACTGAGCTGG GCTCCTCGAG GGGTGGGGCT    420
40
     GCTGTCCCTG GAAGCCTGGC AGCAGCACTG TATCGGGTTG GCTGAAGCTG ARCGCCGTGG    480

     GGTGCAGGGC TCCMGGAATC CCCGTTTGGC TGAAGGGGTT CCCTGTAGCC MGGGATGTTT    540

45   ATGAGGTCTC TCTGATGCCC CAGGCGCAGG ACATGTGTGC GGGTGGAGAA AAGCAGGCCC    600

     TTTCAGTGCC AGCTCCACTC AATTTCTATG TGGACCAAGA ACGATAAACT TAAAAAATTT    660

     TTTTTCCTAA GGTATCTTCA GAATATGGTG TATTTTTATG TGGAAAAGAA AAGTTATGAA    720
50
     GGCAGCTGTT ACTTTAAGAG AAAATTCATT AAAAGTCCTC GAGGTATGAA GATGACGGCG    780

     TGCTTCTCAA TCATTTTGGC ATAACTTGAT TGTGGCTGTA ATTTTTTTTT TTTTTTTTGT    840

55   CAAGCATGTC AGACAATAAA GTCTTTGTAA AAAGRGAAAA AAAAAAAAAA AAAAAAAAAA    900

     ACTCGA                                                              906
```

60

443

(2) INFORMATION FOR SEQ ID NO: 191:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1941 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
CTTCAGCTGA AGCCCAGGGA CCCCTTTTCC ACCCTGGGCC CCAATGCCGT CCTTTCCCCG    60

CAGAGACTGG TCTTGGAAAC CCTCAGCAAA CTCAGCATCC AGGACAACAA TGTGGACCTG    120

ATTCTGGCCA CACCCCCCTT CAGCCGCCTG GAGAAGTTGT ATAGCACTAT GGTGCGCTTC    180

CTCAGTGACC GAAAGAACCC GGTGTGCCGG AGATGGCTGT GGTACTGCTG GCCAACCTGG    240

CTCAGGGGGA CAGCCTGGCA GCTCGTGCCA TTGCAGTGCA GAAGGGCAGT ATCGGCAACC    300

TCCTGGGCTT CCTAGAGGAC AGCCTTGCCG CCACACAGTT CCAGCAGAGC CAGGCCAGCC    360

TCCTCCACAT GCAGAACCCA CCCTTTGAGC CAAYTAGTGT GGACATGATG CGGCGGGCTG    420

CCCGCGCGCT GCTTGCCTTG GCCAAGGTGG ACGAGAACCA CTCAGAGTTT ACTCTGTACG    480

AATCACGGCT GTTGGACATC TCGGTATCAC CGTTGATGAA CTCAKTGGTT TCACAAGTCA    540

TTTGTGATGT ACTGTTTTTG NATTGGCCAG TCATGACAGC CGTGGGACAC CTCCCCCCCC    600

CGTGTGTGTG TGCGTGTGTG GAGAACTTAG AAACTGACTG TTGCCCTTTA TTTATGCAAA    660

ACCACCTCAG AATCCAGTTT ACCCTGTGCT GTCCAGCTTC TCCCTTGGGA AAAAGTCTCT    720

CCTGTTTCTC TCTCCTCCTT CCACCTCCCC TCCCTCCATC ACCTCACGCC TTTCTGTTCC    780

TTGTCCTCAC CTTACTCCCC TCAGGACCCT ACCCCACCCT CTTTGAAAAG ACAAAGCTCT    840

GCCTACATAG AAGACTTTTT TTATTTTAAC CAAAGTTACT GTTGTTTACA GTGAGTTTGG    900

GGAAAAAAAA TAAAATAAAA ATGGCTTTCC CAGTCCTTGC ATCAACGGGA TGCCACATTT    960

CATAACTGTT TTTAATGGTA AAAAAAAAAA AAAAAATAC AAAAAAAAT TCTGAAGGAC    1020

AAAAAAGGTG ACTGCTGAAC TGTGTGTGGT TTATTGTTGT ACATTCACAA TCTTGCAGGA    1080

GCCAAGAAGT TCGCAGTTGT GAACAGACCC TGTTCACTGG AGAGGCCTGT GCAGTAGAGT    1140

GTAGACCCTT TCATGTACTG TACTGTACAC CTGATACTGT AAACATACTG TAATAATAAT    1200

GTCTCACATG GAAACAGAAA ACGCTGGGTC AGCAGCAAGC TGTAGTTTTT AAAAATGTTT    1260

TTAGTTAAAC GTTGAGGAGA AAAAAAAAAA AGGCTTTTCC CCCAAAGTAT CATGTGTGAA    1320

CCTACAACAC CCTGACCTCT TTCTCTCCTC CTTGATTGTA TGAATAACCC TGAGATCACC    1380

TCTTAGAACT GGTTTTAACC TTTAGCTGCA GCGNCTACGT CNAWCGNTGT GTATATATAT    1440

GACGTKGTAC ATTGCACATA CCCTTGGATC CCCACAGTTK GGTCCTCCTC CCAGCTACCC    1500
```

```
CTTTATAGTA TGACGAGTTA ACAAGTTGGT GACCTGCACA AAGCGAGACA CAGCTATTTA      1560

ATCTCTTGCC CAGATATCGC CCCTCTTGGT GCGATGCTGT ACAGGTCTCT GTAAAAAGTC      1620

CTTGCTGTCT CAGCAGCCAA TCAACTTATA GTTTATTTTT TTCTGGGTTT TTGTTTTGTT      1680

TTGTTTTCTT TCTAATCGAG GTGTGAAAAA GTTCTAGGTT CAGTTGAAGT TCTGATGAAG      1740

AAACACAATT GAGATTTTTT CAGTGATAAA ATCTGCATAT TTGTATTTCA ACAATGTAGC      1800

TAAAACTTGA TGTAAATTCC TCCTTTTTTT CCTTTTTTGG CTTAATGAAT ATCATTTATT      1860

CAGTATGAAA TCTTTATACT ATATGTTCCA CGTGTTAAGA ATAAATGTAC ATTAAATCTT      1920

GGTAAGACTT TAAAAAAAAA A                                                 1941
```

(2) INFORMATION FOR SEQ ID NO: 192:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2118 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
AAATAATAAT AANAATAAAT AAAAATWAAG TGCTTAKTGT AACTCAGCGG ACAGGGCTCC        60

CAGCTGCTCT GGCACGTGGG ACACCYTCCA CCCTGCACAC AACAGGCATG CAAAGAGGAC       120

TGGATATGGT GGGGTAGAGT GCTTCTGGTG TGTTCACTTT AAGAAAACAT CTGCCAAGAG       180

AGAAGAGTGC CCAGGAAAGA CCAGGAAAAT ACAAGTACAT GGCTGCTTCA TACCATATAC       240

CCCAATTCTT TAAAGCAGCA AAAGGCACTT TTTTTTTCAG GCCAGAGTGA ATCTAAAACA       300

AACCTGGCTT TGCTTACAGG GAAGCTGTCC CAGAAGGACT GAGTGATGCC TCTTGTTCCC       360

TAAGGTCTGG AGAGTCTTTG CAAGTTTCCA ACGACATTTC CAACCAGGTG GGAGAGACCA       420

GCAGTTGACG AGACAAGTCA GACCCAAAAA ACGACGCCAA GGTAGTGAGT GGGTGCCTAT       480

TTGGGAGTAG GATGATTTGA GGAAAACAGG AAGAAAAACC GGTCAGAAAG TGGCACTTTG       540

GAAGTGGAAA GCTGTTTGCA AATAGCAACT CTGGCTAAAG CGAAAATGTT AATCAAGTAG       600

AAAGTAAAAT TCAGGATCTT AGAAGCTCAT CCTTCTGATG AGAACTATTT TTTTTTCCGT       660

GAAGGAACTA TTATTACTTT AAAAGTGAGG GTAATTTACA TATGGGGTGT ATATATTCTA       720

AAAATAGTAA TAAAAGTACC TTTTATAAGC AATGTTGTGT GGCTTGTAGA AGAAAGCAGG       780

GAGGAAAAAA AGGCAGGCAA AACTAGTCTA GGTCTAGGCC CTAAAAATGA GCTTCCTTCC       840

CACTTGACTG GAAACGCCCA TGTGATTTCT AGGCTGAAAA TAGGTAGGAT TTAACGAGTA       900
```

```
ACCTAGTTCC CTTCTGTCTC TGATTTCTGA TCAGCTGATG GAGCTGCTAG TAAGAGGGGC    960

CGATCATGCT CCCAGACGAG TCCTTTGGCC TCTTGCTCTC CATCCCAAGC CTGACTCCTT    1020

CAGCAGCAGC CCCCTCCTTC TGTGTCCATC TGATGCAGGC AAGCAGGAGC AGTAAGAGGG    1080

CATCCCATGT TCCAGTTCAC CTTCTATGGG GTGACTARGA GGTTCCCGGT AACTAGGGCA    1140

GCCCARGCCC AGCAGGTTGC AAAAGCAGCT GCAAGCTTCA GAAACCCACT TCCTCCAACA  .  1200

CCAGGGAGGT GGCAGAGAGC CCATCCAAAA GCCCACTGGG AGAGGCATAA GATTCTGTGC    1260

CAGGCCCCCA GGTCCCCTCT GTGTCAGGTA GGCTCTGCTA CTGGCCTCTG AAGTAAAGGC    1320

AAANACAAAC GGGCAGGGCA GGGTGGCAGG AATAAAAAAC TCTGGACAGA AACCCTTTTA    1380

ATAAAGGAAA TTCCACCCCT CCCAATCCTT CCATGGAAGG GTGAGACCTT AATGTGATGT    1440

AAGAGGAAGG TCTTCTCTGG CTTTCAGGGA AACAGCTGCA GCTGAAACTT AGGGGCCCAT    1500

TCCAGGGCAC TTTTCACCAC AGCCAGTGCA GCCGCTCCAA GTGCCACTGT CAGCCCCATC    1560

ACTGCCAATT TCACAAAGCG GTTGGTCCTT GGCTTGGTCA GGACATCTTT TGTTCGATCT    1620

TCAGGCCGCA GAAGTCCCCG AANACCGCTG CCGCAGCACC ATATCAGGCC TCTGCTGGGC    1680

TGATGCCAGC TCAAAGTCTT TGAAAGTAGA GGCTGCCGTC CTCTCAGCTT GCTGTTGGGC    1740

AGCGGCCTCC CGAGCAAGTT CGGATGGGGG AAACTGAACA AAAAGGTCTC CTSTCTGCTG    1800

ATCAGTGTCT CATAGGGCAA GTCCTGAGGG ATCTGGGACA ACAGGTGGTG GACCGAGGCC    1860

ATGTCACAGT CACAGTCCAG GACTTCCTGC TCGCGATACA ACACAATCAC GGCTGCAAAG    1920

TAAATCGGCA TCAGTGGGTG GCAGGCCAGG AAGAAGTCAT ATAACCGCAC GACGTGCCTG    1980

AAGTCAGACA GGACATGCCC AAACCAGGTG ATGAGCCAGC TGAGGGCAAA GATGGTCCCT    2040

ACCTCAGCAC TCTGCATGAA GTCATGGAGC TCTGGATTCA CCTGGTCAAT GATGGGCATC    2100

AGATAGTTTA ATATATGC    2118
```

(2) INFORMATION FOR SEQ ID NO: 193:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1538 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```
CCGGGTTCGG CTCTGTGTCA GCAGCCGGGC GGCGCTCGGG CGGGACATGG CAGCCTGTAC    60

AGCCCGGCGG CCTGGCCGTG GGCAGCCGCT GGTGGTCCCG GTCGCTGACT GNGGCCCGGT    120

GGCCAAGGCC GCTCTGTGCG CGGCCGNAGC TGGAGCCTTC TCGCCAGCGT CGACCACGAC    180
```

446

```
GACGCGGAGG CACCTCTCGT CCCGAAACCG ACCAGAGGGC AAAGTGTTGG AGACAGTTGG     240

TGTGTTTGAG GTGCCAAAAC AGAATGGAAA ATATGAGACC GGGCAGCTTT TCCTTCATAG     300

CATTTTTGGC TACCGAGGTG TCGTCCTGTT TCCCTGGCAG GCCAGACTGT RTGACCGGGA     360

TGTGGCTTCT GCAGCTCCAG AAAAAGCAGA GAACCCTGCT GGCCATGGCT CCAAGGAGGT     420

GAAAGGCAAA ACTCACACTT ACTATCAGGT GCTGATTGAT GCTCGTGACT GCCCACATAT     480

ATCTCAGAGA TCTCAGACAG AAGCTGTGAC CTTCTTGGCT AACCATGATG ACAGTCGGGC     540

CCTCTATGCC ATCCCAGGCT TGGACTATGT CAGCCATGAA GACATCCTCC CCTACACCTC     600

CACTGATCAG GTTCCCATCC AACATGAACT CTTTGAAAGA TTTCTTCTGT ATGACCAGAC     660

AAAAGCACCT CCTTTTGTGG CTCGGGAGAC GCTAAGGGCC TGGCAAGAGA AGAATCACCC     720

CTGGCTGGAG CTCTCCGATG TTCATCGGGA AACAACTGAG AACATACGTG TCACTGTCAT     780

CCCCTTCTAC ATGGGCATGA GGGAAGCCCA GAATTCCCAC GTGTACTGGT GGCGCTACTG     840

TATCCGTTTG GAGAACCTTG ACAGTGATGT GGTACAGCTC CGGGAGCGGC ACTGGAGGAT     900

ATTCAGTCTC TCTGGCACCT TGGAGACAGT GCGAGGCCGA GGGGTAGTGG GCAGGGAACC     960

AGTGTTATCC AAGGAGCAGC CTGCGTTCCA GTATAGCAGC CACGTCTCGC TGCAGGCTTC    1020

CAGTGGGCAC ATGTGGGGCA CGTTCCGCTT TGAAAGACCT GATGGCTCCC ACTTTGATGT    1080

TCGGATTCCT CCCTTCTCCC TGGAAAGCAA TAAAGATGAG AAGACACCAC CCTCAGGCCT    1140

TCACTGGTAG GCCAGCTGAG GCCCCAAGTG CCCAGGCTTG GTCACCGGGA AGAACAACTC    1200

TCATCCCACA ATTGCTGCAG AACTCTTCTC TCCCCATCAT GGGCCACAGT GGGTCTCTTA    1260

ATTTGATTGT GGGGTTCTTT TTGTGGGGAG GGGTGGTATA ACTTTTCTTC AGAAGACCCA    1320

TGTGGGACAC CTCCAAGGCT GGCCTCCTCA TAAGCCCTGC CTACACCATG TTCCAGTAAA    1380

CCTCTCCACC AAGGAACTGT GTTCAGCTGC CACAGGCCTG GAGGAGTTTC CTGGCCTGTC    1440

ACGTGAGGTT TGATCAGTAA ACCAGTGCAS GYTTGGCCAA AAAAAAAAAA AAAAAAAAAA    1500

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACTCGA                            1538
```

(2) INFORMATION FOR SEQ ID NO: 194:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1098 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```
AGACCCTGTC TCAAATAATA ATAATAATAA TAATCTTATT TTGGAGAATA AAGAGACCTS      60

TGGATTTGAG GTGCCATTTG GGTAGAAAGA AAAGACGTTT ACACCGAGAA ATAGTCTGTG     120

TTGCCCTGAA GGAGCAGAGG GATGCATCGC TGGAGGTGAC CTACAGTTGA AGAAGACTCA     180

TTATGACAGA CCTTGTCCTT CTTCCTTGTG GAAAGTGTTT CCTCTGCTGC TACTGCTCAT     240

GAGACTCTTC CCCCTCCCTG TCCCAGGGAA CCAAAGGGCT TTNCTACCAC ACCCTTTCTT     300

NGCCCCCCGC CTCCCATGTC TGCTGTGCCT TTGTACTCAG CAATTCTTNG TTTGCTCCCA     360

TTATCTTCCA GCCGGATACA GAGTGAATAG TTAACCACAC TTAGGTCAAA TAGGATCTAA     420

ATTTTTGTTC CTGCTCCNGT GTAAAGAGGC CAGTGTTTGT GTGTTGCAAG CAGCCTTGGA     480

ATAGTAACTC TTCTCATTTG TTTGGGATCT GGCCAMCAAG TTCCAGAATG ATACACGGAT     540

CAGTGCAGAA GTTCATCAGG CTCTCGGACC TTAGGGCTGT TGGAGAAGGC TTCAGCAGCA     600

GAACTGATGG TKAWKGYTCG TGTTCTCCAT CCTCAACTTT CTTTGCTTCG ATCATACACA     660

AGAATACATT TGGAAGGGCA AAAAATGAAC ACTGTTGTTC ATTGCAGCCG TGTTTTGTGA     720

CACAGATGCA CAGTCTGCTG TGAAGACCTT CTCTCAAGTG GSATYTGGGA GTCCATGCCA     780

GATCATGGTG CTTCATGAGA GACTGACAGC TATCAGGGGT TGTGGCACTT AGTGAGGACT     840

CTCCTCCCCC AGTGTGTGCT GATGACACAT ACACACCTGA CAATAGCTTG AGTCTTCTCT     900

GTTCCTTTTA CTCTGTAGCC AACATACACA TGATTTAAAA CCCTTTCTAA ATATCTATCA     960

TGGTTCATCC TTGTCCAAAT GCAGAGTCAG AGCTATTTGT ACTTCATTAT TATTTCCAAG    1020

GCGAATAGTT GGCTTTCTTT TTGCAAAAAT AATTAAAGTT TTTGTATGTT GCAAAAAAAA    1080

AAAAAAAAAA CTACGTAG                                                  1098
```

(2) INFORMATION FOR SEQ ID NO: 195:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1001 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
GAATTCGGCA CGAGATAGCT TGCATCTCAT CCCAGTAAAA CCACTTATTT ATAACATATC      60

AACGTATTGA CAAGGTTGAA GAGCAAGATT GTTCTGAGGT GAGATGCAAA TTTCAAAGGG     120

GTGAGCACTA ATTGTTCCAG TGATTGTTTA TTTATTGGCT AGGACATAAT TACTCTCTTT     180

GAGGTTACAC ATCTGCCTCC AGGTTCCTGT GTGCTTGTGC CCTTGGGATC AGGCCAGGGC     240

AGACTGTGAT CACTGAGATT CAAACTCCCA GARTAATCAG CAAGAGCTTT CTAGAGACCA     300
```

448

```
AGGCCAGGCC TGATCCCTGA GGGATGCATG AGAAGGCTTG GAATCTCATT CTGCTATGGT      360

GGCTCTCTCT TGATCTTCTT GGAGTAGCAA AAACAGCAAT GTGGGCCCAA TGGTGTGGCC      420

TAAATGATCA CAAAGGTAAA TGAGTAAAGG GCTCAGCAGA TGAGTAAGGA GCCTTGTCCT      480

GAGAAATTAG CACTGGGCTC TGCATTCAGA AACATGTGAT AAGCATTGCC CATTGCACAT      540

TGCCTTTATT GTGTAAGGAC ATGAAATTCC AGTTTTGCAT AGCTAGTGAT GAATACCTGA      600

AGGGAATTGC AGACATATTT TATTTTATTT TTAATTGACA GATGGAATTG TATATATTTA      660

TCATGTACAT AATCATGCTT TAAAATATGT ACATTATGGA ATGGCTAAAT CAAACTAACC      720

TAGGCATTAT CTCATATAAT TGTCATTTTT GTGGCGAGAA GACTAAAAAT CTACCCTTTC      780

AGCATTTTTA AAGAATACAA TGTGTTTTAT TAACAACAGT CACCATTTGG TACACTAGAT      840

CTCTTGAACT TCTTCCTCTT ATCTAACTGA GATCTTGTAA CCTTTGATAA CAGCTCCCAA      900

GCCCTTCCCC AACCACTGCT CCACCCGTGG TAACCACCAT TCTATTCTCA ACTTCCTGGT      960

AATCACCATT CTAGACACAG GGAAGACTCT CTACCCTCTG A                         1001
```

(2) INFORMATION FOR SEQ ID NO: 196:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1443 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```
ATAAACTGAA ATAGGTCATG CAAATATAAA ATATTATTTT TAAATTATTT GTCATAAGAA       60

ACGATGGTGG CCATATTTTG CTTTAATAAT GGAAAAAATG TGGTTAGCAT TCTKTGGAAG      120

GTGGTCATCA GATAGTAGAC ATTTTCTAGG ATTTATTTCT ACCTGCATAT GTGGAAATGT      180

GTACTACTTT AGATTTATWT AATGGCAGCT AACTCAGAGG CATCAAAATG TGCTAATGGT      240

GTAATATGGC CTTTGTCTTG CTGTYCTGTT TTGTARGCCT TCAATCAAGC ARGGGCAGGG      300

CCGTACAGTG AACTTGTCCT TTGSCAGACG CCAGCGTCTG CCCCTGACCC GTCTCCACT      360

CTCTGTGTCC TGGAGGAGGA GCCCCTTGAT GCYTACCCTG ATTCACCTTC TGCGTGCCTT      420

GTACTGAACT GGGAAGAGCC GTGCAATAAC GGATCTGAAA TCCTTGCTTA CACCATTGAT      480

CTAGGAGACA CTAGCATTAC CGTGGGCAAC ACCACCATGC ATGTTATGAA AGATCTCCTT      540

CCAGAAACCA CCTACCGGTG AGTGCAAGGG AGTAGAAATC TGCATCAGCA CATCAGCACT      600

TGGGGATCTA AGTAAACCTC TCGGGGAAAA TGACCAAGTG GATGTCATCT CCCAGCTGTT      660
```

```
TCTAAGAGCC CAGATGTCCA GAGTATTGTC TCACCTTGAT CCCTCAGGCC AGAAGACCTG          720

TGAAAAAGCC ACACTGGTTC AGGGACTCAC TGGACGGTTT TGTGTCCACT TTAACTTGCA          780
```
5
```
CCGTCTCTAC CCCAGAGTGG ACTCAAATCC TCAAGTCATC CTCTGAACAT TGTTGTCAGA          840

AATTATAAAA GGGCTTTGGC AATATGTTAG CCCAAGAATT TGGCTTCTTC CAGAAATTGT          900
```
10
```
GCCGACNTTA ACAGTGGCTT AAATGATGGT AAAACTTTTA AGATTTCTAA AAGGTGGCA           960

TTGGAGATAC GTTGACTTTT ATTAAACMAC CTATAGTTGT TTAATGATTT CTAAAAAAT          1020

ATCTGGAGCT CAGGGGTTCA ACTGAGGGAA CACATGTTGA GRATCATTGT TTATAATTA          1080
```
15
```
AATGCCAGGT AACCCGTTGA AATTATCAAA AACATCTTCC ACGTACCAGA AAGCACCTCA         1140

GAGGATAGTT CTGTTATGGA GAAGATGAAA TGGTTTAGTA GTGTAGGAAC TATGGAAAGG         1200
```
20
```
TGAGCTTAGA TTTGGATAGT AAAACCTCAA GACCCTATTT AAAAAGTATT TTATGAATGC         1260

AGCATAAATA ATTTAATTCA GTGTTAANAT GCCAAGGCTA GTATATTGAG CTGAATGTGA         1320

AAAGAAACTC ACATTGGGAG AATGCCACCT TTTCCTTATA AGATAGCTTT GAAGATACCA         1380
```
25
```
TTTTAGACAG ATGGAAATTG AATAGCTTTA GAAAAGGCAA ATGTTTGATC TTGGGGAAAA         1440

AAA                                                                        1443
```

30

```
(2) INFORMATION FOR SEQ ID NO: 197:
```

35
```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1282 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
```

40
```
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GAAAAAAAAA AGTATGACCC AGTAGCTAGG CACCTGTGGC CCCGCCAAGT TGACACATAA           60
```

```
AATTAACTGT CACAGTATCA TCTTAGAAGT GAAAGAAGCC CCTTTATCCT GCAGTGCCCC          120
```
45
```
TCTACCACCA CCTACTGACA AAGAACATGG TGCTATCTGG CATGGGAGAA ATGTTCAGTT          180

TGCTATGGCT TGTATGTGTC CCCTCAAATT CAAGTGTTGC CAATGTGACA GCATCAAGAG          240
```
50
```
GTGGGGTCTT TAAGAGATCA CTAGGCCATG AGGGATTCTC TTAGGACTGG GATGAAGGCC          300

CATAATAAAA GAGGTTTCAG GGAGCATCCT GCTAGCTTGC CTTCTGTATG TGAGAACACA          360

GCAAGAAAGC CCTAGTCAAC AAGTGCCAGC TCCTTGATCT TAGACTTCCC ATCCTCCAGA          420
```
55
```
ACTGTGAGAA ATACATTTCT GTTCCTTACA AATTACCCAG TCTCCTGTAT TCTGTTATAG          480

CAGCACAAAA TGAAGATACC ATACCTGAAC ACCTGAACAT TCTTCACAG GTAGTAAATG          540
```
60
```
CACTGCTTTA TTCTGGTCTC AGTATTGTGT GCTTAATAAG GAAATGAGAA AGGGTGGATC          600
```

```
AGGGCATAGG ATGAACAAGT TACTGCTAGA CCTCTCACHA TGCCACTAAT GGATAAGATT       660

GTATTTTCAT CATTNCTTGT CTCTTCGGAA GCTAACACTA TGCTATAATA GGCATTAAAT       720

AGATGTCTAA AAACACCTTA AGTATTTGTC TAGAAATCTG GTGCATTGTC CAGAAAGAAC       780

CAAAATTCMA AATAATTTCA AAGGGCCTAA AGCACTATTT AATCAGAATT CATTAGTTTT       840

TAATGGTACT ACCACTCTCA AATTTAAAAT GTCATCTTAC GTTCCTCTTC CTCGCATTGG       900

ATTTATTGCT AAAACCTGGT AAACACTTTA ATCCYTTTCA ATTCCATTAC CACTGCTCTT       960

GTCCAGAATT ACTCGCAGAC TAATAGTCAC CTGACTTCTC CCCCTGCATC CCGATTTGCT      1020

GTCTAATTCT GGTTACAAAT AAGTAACTGC CAAACTAATC TTTCTAAAAA GCAGACTGA       1080

TCTCGTCACT CCTTTGCTCA ACAATGTAAA AGCTCCCATT GTCTCCCAAA TAAAACCAGC      1140

TTTCCACTGT GTATACAATA CATCCATGAT CTGTATCCAG CATCATTTTG TATTTGCTCA      1200

CTTTATACAC CACCCCCCAT GCCACATCAA ATTAAATTAT CCTGATAAAT GCAACTGCAA      1260

AAAAAAAAAA AAAAAAACTC GA                                              1282
```

(2) INFORMATION FOR SEQ ID NO: 198:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 951 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```
ATTTCGGAAC GAGGACTGAA GTGGGAGCGG CGGCAGGGTA GAAGACAGAA GGGGGATCTA        60

TGTGGTAACT AAAGAATGTT TCTGTTTTGT TAATTATTGT GTGTGTGTGG TTTTATTGTT       120

TGCTTAAGAG AATCAAAAAC TGAAAAAAAT GAGAATACAG GAAATGGCTC TTGTTTATTT       180

TTTTGCTGTG TTTACAGCTT GTTAATGCTC TACTGTCTTT GTTTCAAGAG AGATTTGTTC       240

ACTGCCCAGC TCGTTTTGTG TCCTGAGCCC TATGCCCAGC CCACCTTATA AATCATGCCT       300

GTTTAGATGT TTGATTTTGT TCTGTTTGCT ATTGTTATCT TAAAGGTGTA TAACTCTGAC       360

ATGCCAGACA TCAAATTAAG CTCAAATTAA GCTCTCGTTT AAATGTTTAA ACACCTAATT       420

TATATTCTAA TTGATCCCAG CCACTGATGC ATGTACTTTA GCTACTTCTG CTAAATAAGC       480

ATATTAATTT TCCACATCAG GCCATCAGAT CTTGAGAACC AACAGTTATC TAGAATTCCG       540

TGTCTACTAA TGTTTCACCT GCATGCAGCC TTCATTAATT TTGTAGCAAA ATATAAAGTG       600

ATCATTATGT AGTTTCTGGA TTAAAAAAAT TTGTGTGTGA AGTTGCTTTG TAAAGTGCAT       660
```

451

```
GTGGAATTAA TGGGACAGTG TGCCCTTTGT GTTAGATGTT AGAGCAAAAG AAAGGGCTTA      720

TAGTGTTAGT ATTGGAGCAC TTTGAAGATA GATATTTTCA GAAAAGATGT AGGATTTAAA      780

AGTTAAATTT TAAATTTTAG AAAAAGATAT GATGGCAATT GGAAATAGTC ACAATGAAGT      840

TCTTCATCCA GTAGGTGTTT AACAGTGTTA TTTTGCCACT GGTAATGTGT AAACTGTGAG      900

TGATTTACAA TAAATGATTA TGAATTCAAA AAAAAAAAAA AAAAAACTCG A              951
```

(2) INFORMATION FOR SEQ ID NO: 199:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1740 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
TTATTATAAT AATGATGATG ATTCCAAGGA AAAAACCTAC AGCGAATGTT CCATTTCTAC      60

CCCGCACGCA GACACTCTCC CTAACACTGA TAACCTGAGC CCCCAGCACT GGACGGAAGA      120

ATGCTGGCGT CTCCGTGTGT ACTGGTTCAG GGTTCTGGCC CCAGCCTTGT CAGGACCCCC     180

TGGTGTCCAG AGCCCCCACC CCTCCCGCAA CAAGCAGCTG ATGCCCCAGT GATTCTCTAT     240

ACATTTTTCA CCTCGGCCAA TATGTCCAGG AAAACTGCTT ACTTCTCTTT TCTTGCCTGG     300

AGCCTTCATT GTTCACCCTT ACGTTGCAAT ATAGGAATTA ATGCTACAAA ATAAAAGTAA     360

AGCTTACCTG AAAAGTGCAT AGTTTGGGGC AATGGTATCT ACATCTCCCA CTGTGGGAAA     420

ACCAGCAAAG CATCAAAACT CTCAATTCTC CTGTTACCRA ATGCAGATCT GAATTATAAG     480

ATGTTTATGT TTGACCATTG TTTCAACAAT GGGATTTTGT TACGAATTAT CCCTTTAACT     540

GAAACCCTCA GTTTTACTGT TTACATTATT AGGAAAACAG GGATATCTTT TGAATCTAAA     600

AATTTGATGT ACAGCATGTG ATTTTTGAAG TTTACATGTA AAGTCACAGT ATAGGTGAAA     660

TAACGTTTGT CATATTTTGA GACGTATCCT GCAGCCATGT TTTTACGTGA GTGTTTTAGT     720

CAAAGTACAT GGTAGACAGT CTTTCACAAT AAAAGGAAAA GGATTTTTTT TCCTCCAAAT     780

GTACATTTAT CAACCTAATG ATTGATTTTT TTAAAAAGAG ATTTCGCCCC AGTCTGGTTT     840

ATGAAAGTTC ATTGCCCTAA ACTGTGCTGA TTGTTTTTAA TCAAGTTATA AATTTCCAAC     900

CTAGATCATG TATCTACCAA CTCTCCTGCA TTTTCCAAAA GGCATTGAGC TTAAATATTA     960

GTCTTGCTTA GAGTAGGTTA TCCACTTACA TGCTGCGCTA AAGCCATGCC TTTGAAACTC     1020

CTTGTTTAAA ACATGATATG ATTTTTGTGG GCAGTTTCAG AAAAGAAAAC AAACAAACAA     1080

AAATCGACCC TTTAATTATT ACTTGCAACT CAACAGATCT CCCTGCCGTA CTGCCTTTTC     1140
```

```
CAGGAACTTT ACTTCAGGGC TGTCCAGATT GCAGTTGTGC CCCGTGTATG TGGATCTAGT    1200

TCACAGAGTC TTTGGAAGCC AGCAGTCGTG CCCTCCGTAT ACTGTCCACT CATTTTATGT    1260

AGATTTGGTA TCCTCAGCAG CCAGTGTTAA CACCACTGTC ACGTAGTTAN CAGATTCATC    1320

TTTTATGTAT TTAAAGTAAT CCATACTATG ATTTGGTTTT TCCCTGCACC ATTAATTCTG    1380

GCATCAGATC AGTTTTTGTG TTGTGAAGTT CTACTGTGGT TTGACCCAAG ACCACAACCA    1440

TGAGACCCTG AAGTAAAGAT AAGGTACACA TACATTATTT GAGTAACTGT TTCCTTGGGG    1500

GCCAATCTGT GTATGCTTTT AGAAGTTTAC AGAATGCTTT TATTTTTGTC TATAACAAAC    1560

AGTCTGTCAT TTATTTCTGT TGATAAACCA TTTGGACAGA GTGAGGACGT TTGCCCTGTT    1620

ATCTCCTAGT GCTAACAATA CACTCCAGTC ATGAGCCGGG CTTTACAAAT AAAGCACTTT    1680

TGATGACTCA MAAAAAAAAA AAAAAAAAMC YCGGGGGGGG GCCGGTAACC CATTTNNCCC    1740
```

(2) INFORMATION FOR SEQ ID NO: 200:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1707 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```
GCTTATAGAA GGGAGAGGAG CGAACATGGC AGCGCGTTGG CGGTTTTGGT GTGTCTCTGT      60

GACCATGGTG GTGGCGCTGC TCATCGTTTG CGACGTTCCC TCAGCCTCTG CCCAAAGAAA     120

GAAGGAGATG GTGTTATCTG AAAAGGTTAG TCAGCTGATG GAATGGACTA ACAAAAGACC     180

TGTAATAAGA ATGAATGGAG ACAAGTTCCG TCGCCTTGTG AAAGCCCCAC CGAGAAATTA     240

CTCCGTTATC GTCATGTTCA CTGCTCTCCA ACTGCATAGA CAGTGTGTCG TTTGCAAGCA     300

AGCTGATGAA GAATTCCAGA TCCTGGCAAA CTCCTGGCGA TACTCCAGTG CATTCACCAA     360

CAGGATATTT TTTGCCATGG TGGATTTTGA TGAAGGCTCT GATGTATTTC AGATGCTAAA     420

CATGAATTCA GCTCCAACTT TCATCAACTT TCCTGCAAAA GGGAAACCCA AACGGGGTGA     480

TACATATGAG TTACAGGTGC GGGGTTTTTC AGCTGAGCAG ATTGCCCGGT GGATCGCCGA     540

CAGAACTGAT GTCAATATTA GAGTGATTAG ACCCCCAAAT TATGCTGGTC CCCTTATGTT     600

GGGATTGCTT TTGGCTGTTA TTGGTGGACT TGTGTATCTT CGAAGAGTAA TATGGAATTT     660

CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT TTGTGCTTGC TATGACATCT     720

GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA     780
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```
CATGTGAATT ATATCCATGG AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT    840

CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT    900

GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA    960

TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC ATGGCTACCC ATACAGCTTT    1020

CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC    1080

GAAAATCGTG TGTGTTTGAA AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT    1140

TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC    1200

AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA    1260

GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT ATTATAAAAA TTGTAAAACT    1320

ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT    1380

TTTATATTGC CTTATCCAAA GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG    1440

CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT    1500

GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG    1560

AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC AGCAAGACAG TTGTTTCTCC    1620

TCCTCCTTGC ATATTTCCTA CTGAAATACA GTGCTGTCTA TGATTGTTTT TGTTTTGTTG    1680

TTTTTTYGAG ATCACGYTAC TGGGCTC                                        1707
```

(2) INFORMATION FOR SEQ ID NO: 201:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 779 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```
CTGTCCCCAG TGTTTCCAGG TAATGACTTG GCACTCCAGA GAAAGTTTCA TRCTGTTGCG    60

TGTGGTGGCT CCAAGCCAAG CACCTGGCAT GCAGGTCAGC CCTTCCCAGC GGGCGTGGCG    120

TCGTCCTCTT CACAGATGCC ACGTTGCAGC CCCAAGGCCT CACCATTTTG CGTTTTTTAG    180

AAACCCATTT TCTTGGTCAT TTATAAAGCT GCTTTATAGA TATCTTTGAT CCTGGCATGC    240

CTTGGTTTCC TCTCCCTTCC CTCTTTCCAA TCCTGGTTTC CTAACCTCCT CTTGTAGTAA    300

TTCTCAACTC AACTCAAAGT CCCAAGAATT TGGAATGGTA GGATGCTGTG CGGGGAGCTC    360

GAGGCTGAGG CATAATCACT GCTTCGGTTC TGCTCATCAG GGGACACGCT CCCTTACTCA    420

TGGCAGCCAT GTTTGATTGT CACAGAGCCC CCCGAATACT CTGTCTATAG TGACACACTG    480
```

454

```
      TAGGTGTCAT AAATTTTAAG AAACCTGCTT TTAAGTACTA TTTATAGGTT TTTCTGTTAT        540

5     ACTTGCAACC TAGTTTTAAA ATACATGAGG ATTTTATGAA AGCTTTATAC AGACATTTAT        600

      AGGAAACTCA TTCTTTGATT TTAGGTGCCA TTTAAATTGA TAACACTTAC TTTATAAAAA        660

      GATGCTTTTT GTCTGGATAG AGCCTTATAG TTTAAAATAT CTTCATATAT TGCCATTTGA        720

10    TCAAATAAAT TTCTTACTTA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAACTCGA         779
```

15   (2) INFORMATION FOR SEQ ID NO: 202:

             (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1617 base pairs
                   (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```
25    GGCACAGCTT TCTGTCTCTT CCTCGCTCCC TCTCTTTCTC TCCTCCCTCT GCCTTCCCAG         60

      TGCATAAAGT CTCTGTCGCT CCCGGAACTT GTTGGCAATG CCTATTTTTT GGCTTTCCCC        120

      CGCGTTCTCT AAACTAACTA TTTAAAGGTC TGCGGTCGCA AATGGTTTGA CTAAACGTAG        180

30    GATGGGACTT AAGTTGAACG GCAGATATAT TTCACTGATC CTCGCGGTGC AAATAGCGTA        240

      TCTGGTGCAG GCCGTGAGAG CAGCGGGCAA GTGCGATGCG GTCTTCAAGG GCTTTTCGGA        300

35    CTGTTTGCTC AAGCTGGGCG ACACATGGCC AACTACCCGC AGCCTGGGAC GACAAGACGA        360

      ACATCAAGAC CGTGTGCACA TACTGGGAGG ATTTCCACAG CTGCACGGTC ACAGCCCTTA        420

      CGGATTGCCA GGAAGGGGCG AAAGATATGT GGGATAAACT GAGAAAAGAA TCCAAAAACC        480

40    TCAACATCCA AGGCAGCTTA TTCGAACTCT GCGGCAGCGG CAACGGGGCG GCGGGGTCCC        540

      TGCTCCCGGC GTTCCCGGTG CTCCTGGTGT CTCTCTCGGC AGCTTTAGCG ACCTGGCTTT        600

45    CCTTCTGAGC GTGGGGCCAG CTCCCCCCGC GCGCCCACCC ACACTCACTC CATGCTCCCG        660

      GAAATCGAGA GGAAGATCCA TTAGTTCTTT GGGGACGTTG TGATTCTCTG TGATGCTGAA        720

      AACACTCATA TAGGATTGTG GGAAATCCTG ATTCTCTTTT TTATTTCGTT TGATTTCTTG        780

50    TGTTTTATTT GCCAAATGTT ACCAATCAGT GAGCAAGCAA GCACAGCCAA AATCGGACCT        840

      CAGCTTTAGT CCGTCTTCAC ACACAAATAA GAAAACGGCA AACCCACCCC ATTTTTTAAT        900

55    TTTATTATTA TTAATTTTTT TTGTTGGCAA AAGAATCTCA GGAACGGCCC TGGGCACCTA        960

      CTATATTAAT CATGCTAGTA ACATGAAAAA TGATGGGCTC CTCCTAATAG GAAGGCGAGG       1020

      AGAGGAGAAG GCCAGGGGAA TGAATTCAAG AGAGATGTCC ACGGACGAAA CATACGGTGA       1080
60
```

455

```
ATAATTCACG CTCACGTCGT TCTTCCACAG TATCTTGTTT TGATCATTTC CACTGCACAT    1140

TTCTCCTCAA GAAAAGCGAA AGGACAGACT GTTGGCTTTG TGTTTGGAGG ATAGGAGGGA    1200

GAGAGGGAAG GGGCTGAGGA AATCTCTGGG GTAAGAGTAA AGGCTTCCAG AAGACATGCT    1260

GCTATGGTCA CTGAGGGGTT AGCTTTATCT GCTGTTGTTG ATGCATCCGT CCAAGTTCAC    1320

TGCCTTTATT TTCCCTCCTC CCTCTTGTTT TAGCTGTTAC ACACACAGTA ATACCTGAAT    1380

ATCCAACGGT ATAGATCACA AGGGGGGGAT GTTAAATGTT AATCTAAAAT ATAGCTAAAA    1440

AAAGATTTTG ACATAAAAGA GCCTTGATTT TAAAAAAAAA AGAGAGAGAG ATGTAATTTA    1500

AAAAGTTTAT TATAAATTAA ATTCAGCAAA AAAAGATTTG CTACAAAGTA TAGAGAAGTA    1560

TAAAATAAAA GTTATTGTTT GAAAAAAAAA AAAAAAAAAW CTCGACCGCA AGGGAAT      1617
```

(2) INFORMATION FOR SEQ ID NO: 203:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1974 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```
GAATTCGGCA CGAGGCTGAG GGAGCTGCAG CGCAGCAGAG TATCTGACGG CGCCAGGTTG     60

CGTAGGTGCG GCACGAGGAG TTTTCCCGGC AGCGAGGAGG TCCTGAGCAG CATGGCCCGG    120

AGGAGCGCCT TCCCTGCCGC CGCGCTCTGG CTCTGGAGCA TCCTCCTGTG CCTGCTGGCA    180

CTGCGGGCGG AGGCCGGGCC GCCGCAGGAG GAGAGCCTGT ACCTATGGAT CGATGCTCAC    240

CAGGCAAGAG TACTCATAGG ATTTGAAGAA GATATCCTGA TTGTTTCAGA GGGGAAAATG    300

GCACCTTTTA CACATGATTT CAGAAAAGCG CAACAGAGAA TGCCAGCTAT TCCTGTCAAT    360

ATCCATTCCA TGAATTTTAC CTGGCAAGCT GCAGGGCAGG CAGAATACTT CTATGAATTC    420

CTGTCCTTGC GCTCCCTGGA TAAAGGCATC ATGGCAGATC CAACCGTCAA TGTCCCTCTG    480

CTGGGAACAG TGCCTCACAA GGCATCAGTT GTTCAAGTTG GTTTCCCATG TCTTGGAAAA    540

CAGGATGGGG TGGCAGCATT TGAAGTGGAT GTGATTGTTA TGAATTCTGA AGGCAACACC    600

ATTCTCCAAA CACCTCAAAA TGCTATCTTC TTTAAAACAT GTCAACAAGC TGAGTGCCCA    660

GGCGGGTGCC GAAATGGAGG CTTTTGTAAT GAAAGACGCA TCTGCGAGTG TCCTGATGGG    720

TTCCACGGAC CTCACTGTGA GAAAGCCCTT GTACCCCAC GATGTATGAA TGGTGGACTT    780

TGTGTGACTC CTGGTTTCTG CATCTGCCCA CCTGGATTCT ATGGAGTGAA CTGTGACAAA    840

GCAAACTGCT CAACCACCTG CTTTAATGGA GGGACCTGTT TCTACCCTGG AAAATGTATT    900
```

456

```
TSCCCTCCAG GACTAGAGGG AGAGCAGTGT GAAATCAGCA AATGCCCACA ACCCTGTCGA        960

AATGGAGGTA AATGCATTGG TAAAAGCAAA TGTAAGTKTT CCAAAGGTTA CCAGGGAGAC       1020

CTCTGTTCAA AGCCTGTCTG CGAGCCTGGC TGTGGTGCAC ATGGAACCTG CCATGAACCC       1080

AACAAATGCC AATGTCAAGA AGGTTGGCAT GGAAGACACT GCAATAAAAG GTACGAAGCC       1140

AGCCTCATAC ATGCCCTGAG GCCAGCAGGC GCCCAGCTCA GGCAGCACAC GCCTTCACTT       1200

AAAAAGGCCG AGGAGCGGCG GGATCCACCT GAATCCAATT ACATCTGGTG AACTCCGACA       1260

TCTGAAACGT TTTAAGTTAC ACCAAGTTCA TAGCCTTTGT TAACCTTTCA TGTGTTGAAT       1320

GTTCAAATAA TGTTCATTAC ACTTAAGAAT ACTGGCCTGA ATTTTATTAG CTTCATTATA       1380

AATCACTGAG CTGATATTTA CTCTTCCTTT TAAGTTTTCT AAGTACGTCT GTAGCATGAT       1440

GGTATAGATT TTCTTGTTTC AGTGCTTTGG GACAGATTTT ATATTATGTC AATTGATCAG       1500

GTTAAAATTT TCAGTGTGTA GTTGGCAGAT ATTTTCAAAA TTACAATGCA TTTATGGTGT       1560

CTGGGGGCAG GGGAACATCA GAAAGGTTAA ATTGGGCAAA AATGCGTAAG TCACAAGAAT       1620

TTGGATGGTG CAGTTAATGT TGAAGTTACA GCATTTCAGA TTTTATTGTC AGATATTTAG       1680

ATGTTTGTTA CATTTTTAAA AATTGCTCTT AATTTTTAAA CTCTCAATAC AATATATTTT       1740

GACCTTACCA TTATTCCAGA GATTCAGTAT TAAAAAAAAA AAAATTACAC TGTGGTAGTG       1800

GCATTTAAAC AATATAATAT ATTCTAAACA CAATGAAATA GGGAATATAA TGTATGAACT       1860

TTTTGCATTG GCTTGAAGCA ATATAATATA TTGTAAACAA AACACAGCTC TTACCTAATA       1920

AACATTTTAT ACTGTTTGTA TGTATAAAAT AAAGGTGCTG CTTTAGTTTT CTGA            1974
```

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(2) INFORMATION FOR SEQ ID NO: 204:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1057 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CGGCCTTCCG GGGCAACCGT TCGTCCCAAC NCGGGAAAGG GTCCTGGAGN CGGGAACTAG        60

GAGCCTCGGA AGTCCAAGGG CGGAGCGCCC TTTGCTAATA AGCCAATCAG AACGTGAGAC       120

GCTCCGGTGG GNCGGTGCCG TCGAGCGCGG GGTGGAGTCT GGGTGACTTG GCTGGCGGGA       180

TCAAGTGCAG CTGCTTCAGG CTGAGGTGGC AGATAGTGAG CGCTGGTGGC GGAGTTAAAG       240

TYAAAGCAGG AGAGTAATWA TGAATAGCGC AGCGGGATTC TCACACCTAG ACCGTCGCGA       300
```

457

```
GCGGGTTCTC AAGTTAGGGG AGAGTTTCGA GAAGCAGCCG CGCTGCGCTT CCACACTGTG        360

CGCTATGACT TCAAACCTGC TTCTATTGAC ACTTCTTCTG AAGGATACCT TGAGKTTGGC        420

GAAGKTGAAC AGKTGACCAT WACTCTGCCM AATATAGAAA GTTGAAGGAA GCAGTAAAAT        480

TCAGTATCGT AAAGAACAAC AGCAACAACA ATGTGGAATT CASCCAGGAC TCCCAATCTT        540

GTAAAACATT CTCCATCTGA AGATAAGATG TCCCCAGCAT CTCCAATAGA TGATATCGAA        600

AGAGAACTGA AGGCAGAAGC TAGTCTAATG GACCAGATGA GTAGTTGTGA TAGTTCATCA        660

GATTCCAAAA GTTCATCATC TTCAAGTAGT GAGGATAGTT CTAGTGACTC AGAAGATGAA        720

GATTGCAAAT CCTCTACTTC TGATACAGGG NAATTGTGTC TCAGGACATC CTACCATGAC        780

ACAGTACAGG ATTCCTGATA TAGATGCCAG TCATAATAGA TTTCGAGACA ACAGTGGCCT        840

TCTGATGAAT ACTTTAAGAA ATGATTTGCA GCTGAGTGAA TCAGGAAGTG ACAGTGATGA        900

CTGAAGAAAT ATTTAGCTAT AAATAAAAAT TTATACAGCA TGTATAATTT ATTTTGTATT        960

AACAATAAAA ATTCCTAAGA CTGAGGGAAA TATGTCTTAA CTTTTGATGA TAAAAGAAAT       1020

TAAATTTGAT TCAGAAAAAA AAAAAAAAAA AACTCGA                                1057
```

(2) INFORMATION FOR SEQ ID NO: 205:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 721 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
GAATTCGGCA CGAGTCATCC CTCTCCCTCT TTCACTCCCT TACTCTTACT CTGTTTTTTG         60

TGCTCCAGAC AGACAGACCC TACCTCTTTT GCTTCTTTTT TGTTTGTTTG TTTTGAGATG        120

GAGTGTCGCT CTTGTTGCCC AGGCTGGAGT GCAGTGGCGC AATCTCGGCT CACCACAACC        180

TCTGCCTCCC GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CCGAGAAGCT GGGGATTACA        240

GGCATGCGCC ACCACACCCA GCTNAATTTT ATATTTTTAG TAGAGATGGT GTTTCTCCAT        300

GTTGGTCAGG CTGGCCTCAA ACTCCCAACC TCAGGTGATN CCGCCTGCTT TGGCCTCCCC        360

AAAGTGCTGG GATTACAGGC GTGAGCCACT GCGCCCAGCC TCTTTTGCTC CTTTATACTC        420

ATTAACTCAC GCCTGTAATC CCTGTTTTGG GAGGCCAAAG TGAGAAGGTT GCTTGAGGCC        480

AAGAGTTTGA GACTAGCCTG GCAACACAG CAAGATGCCA TCTTTATAAT AAAAATAAAA        540

ATAAAAATCA ATTAGCTGGG CATGGTGGAA CGCACCTGTA GTCCCAGCCA ATTGAGAGGC        600

TGAAGTGGGA GGATCATTGA GCCCAGGAGT TGAGGTTGCA GTGAGCCATG ATCATGTCAC        660
```

458

TACACTCAGC CTGGGCAATA GAGGGACATG TTGTCTCTAA AAAAAAAAAA AAAAAACTCG   720

A   721

(2) INFORMATION FOR SEQ ID NO: 206:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2465 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCACCATTTA TCCAACTGAA GAGGAGTTAC AGGCAGTTCA GAAAATTGTT TCTATTACTG   60

AACGTGCTTT AAAACTCGTT TCAGACAGTT TGTCTGAACA TGAGAAGAAC AAGAACAAAG   120

AGGGAGATGA TAAGAAAGAG GGAGGTAAAG ACAGAGCTTT GAAAGGAGTT TTGCGAGTGG   180

GAGTATTGGC AAAAGGATTA CTTCTCCGAG GAGATAGAAA TGTCAACCTT GTTTTGCTGT   240

GCTCAGAGAA ACCTTCAAAG ACATTATTAA GCCGTATTGC AGAAAACCTA CCCAAACAGC   300

TTGCTGTTAT AAGCCCTGAG AAGTATGACA TAAAATGTGC TGTATCTGAA GCGGCAATAA   360

TTTTGAATTC ATGTGTGGAA CCCAAAATGC AAGTCACTAT CACACTGACA TCTCCAATTA   420

TTCGAGAAGA GAACATGAGG GAAGGAGATG TAACCTCGGG TATGGTGAAA GACCCACCGG   480

ACGTCTTGGA CAGGCAAAAA TGCCTTGACG CTCTGGCTGC TCTACGCCAC GCTAAGTGGT   540

TCCAGGCTAG AGCTAATGGT CTGCAGTCCT GTGTGATTAT CATACGCATT CTTCGAGACC   600

TCTGTCAGCG AGTTCCAACT TGGTCTGATT TTCCAAGCTG GGCTATGGAG TTACTAGTAG   660

AGAAAGCAAT CAGCAGTGCT TCTAGCCCTC AGAGCCCTGG GGATGCACTG AGAAGAGTTT   720

TTGAATGCAT TTCTTCAGGG ATTATTCTTA AAGGTAGTCC TGGACTTCTG GATCCTTGTG   780

AAAAGGATCC CTTTGATACC TTGGCAACAA TGACTGACCA GCAGCGTGAA GACATCACAT   840

CCAGTGCACA GTTTGCATTG AGACTCCTTG CATTCCGCCA GATACACAAA GTTCTAGGCA   900

TGGATCCATT ACCGCAAATG AGCCAACGTT TTAACATCCA CAACAACAGG AAACGAAGAA   960

GAGATAGTGA TGGAGTTGAT GGATTTGAAG CTGAGGGGAA AAAAGACAAA AAAGATTATG   1020

ATAACTTTTA AAAAGTGTCT GTAAATCTTC AGTGTTAAAA AAACAGATGC CCATTTGTTG   1080

GCTGTTTTTC ATTCATAATA ATGTCTACAT TGAAAAATTT ATCAAGAATT TAAAGGATTT   1140

CATGGAAGAA CCAAGTTTTT CTATGATATT AAAAAATGTA CAGTGTTAGG TATTATTTGA   1200

ATGGAAAGAC ACCCAAAAAA AAAATGTGC TCCGACTAGG GGGAAAACAG TAGTTCCGAT   1260

459

```
        TTTTTCCCAT TATTTTTATT TTATTTTCTG GTTGCCCTAG CTTCCCCCCC TATTTTTGTG        1320

        TCTTTTATTA ACTAGTGCAT TGTCTTATTA AATCTTCACT GTATTTAATG CAGGATGTGT        1380

 5      GCTTCAGTTG CTCTGTGTAT TTTGATATTT TAATTTAGAG GTTTTGTTTG CTTTTTGACA        1440

        CTAGTTGTAA GTTACTTTGT TATAGATGGT ATCCTTTACC CCTTCTTAAT ATTTTACAGC        1500

        AGTACGTTTT TTTGTAACGT GAGACTGCAG AGTTTGTTTT TCTATATGTG AAGGATTACA        1560

 10     ACACAAAAG TTATCCTGCC ATTCGAGTGC TCAGAACTGA ATGTTTCTGC AGATCTTGTG         1620

        GCATTTGTCT CTAGTGTGAT ATATAAAGGT GTAATTAAGA CAGAGTTCTG TTAATCTAAT        1680

 15     CAAGTTTGCT GTTAGTTGTG CATTAGCAGT ATAAAAGCTA ATATATACTA TATGGTCTTG        1740

        CAACAGTTTT AAAGCCTCTG CATAATTGAT AATAAAAATG CATGACATTC TTGTTTTTAA        1800

        TAGACTTTTA AAATCATAAT TTTAGGTTTA ACACGTAGAT CTTTGTACAG TTGACTTTTT        1860

 20     GACATAGCAA GGCCAAAAAT AACTTTCTGA ATATTTTTTT CTTGTGTATA AGTGGAAAGG        1920

        GCATTTTTCA CATATAAGTG GGCTAACCAA TATTTTCAAA AGAACTTCAT CATTGTACAA        1980

 25     CTAACAACAG TAACTAGCCC TTAATTATGG TGACAGTTCC TTATTGGTGT GTGTGAGATT        2040

        ACTCTAGCAA CTATTACAGT ATAACACAGA TGATCTTCTC CACACACCCC ATCACCCAGA        2100

        TAATTTACAG TTCTGTTAAC AGTGAGGTTG ATAAAGTATT ACTGATAAAA AATTATCTAA        2160

 30     GGAAAAAAAC AGAAAATTAT TTGGTGTGGC CATCTTACCT GCTTATGTCT CCTACACAAA        2220

        GCTAAATATT CTAGCAGTGA TGTAATGAAA AATTACATCT TACTGTTGAT ATATGTATGC        2280

 35     TCTGGTACAC AGATGTCATT TTGTTGTCAC AGCACTACAG TGAAATACAC AAAAAATGAA        2340

        ATTCATATAA TGACTTAAAT GTATTATATG TTAGAATTGA CAACATAAAC TACTTTTGCT        2400

        TTGAAATGAT GTATGCTTCA GTAAAATCAT ATTCAAATTT AAAAAAAAAA AAAAAAAAAA        2460

 40     CTCGA                                                                   2465
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45

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        (2) INFORMATION FOR SEQ ID NO: 207:

              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1480 base pairs
 50                (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:
 55
        GAATTCGGCA CGAGCTCAAG CTGGCAGGTG GTCGGGGGAG CGGCCGGAGA GGAGCTGCCG        60

        GGAGTTCGTG CCCTGCAGGA CATGACACCA GTGGCATATC ACGGCCATGG GGTCTCAGCA        120

 60     TTCCGCTGCT GCTCGCCCCT CCTCCTGCAG GCGAAAGCAA GAAGATGACA GGGACGGTTT        180
```

```
GCTGGCTGAA CGAGAGCAGG AAGAAGCCAT TGCTCAGTTC CCATATGTGG AATTCACCGG    240

GAGAGATAGC ATCACCTGTC TCACGTGCCA GGGGACAGGC TACATTCCAA CAGAGCAAGT    300

AAATGAGTTG GTGGCTTTGA TCCCACACAG TGATCAGAGA TTGCGCCCTC AGCGAACTAA    360

GCAATATGTC CTCCTGTCCA TCCTGCTTTG TCTCCTGGCA TCTGGTTTGG TGGTTTTCTT    420

CCTGTTTCCG CATTCAGTCC TTGTGGATGA TGACGGCATC AAAGTGGTGA AAGTCACATT    480

TAATAAGCAA GACTCCCTTG TAATTCTCAC CATCATGGCC ACCCTGAAAA TCAGGAACTC    540

CAACTTCTAC ACGGTGGCAG TGACCAGCCT GTCCAGCCAG ATTCAGTACA TGAACACAGT    600

GGTGAATTTT ACCGGGAAGG CCGAGATGGG AGGACCGTTT TCCTATGTGT ACTTCTTCTG    660

CACGGTACCT GAGATCCTGG TGCACAACAT AGTGATCTTC ATGCGAACTT CAGTGAAGAT    720

TTCATACATT GGCCTCATGA CCCAGAGCTC CTTGGAGACA CATCACTATG TGGATTGTGG    780

AGGAAATTCC ACAGCTATTT AACAACTGCT ATTGGTTCTT CCACACAGCG CCTGTAGAAG    840

AGAGCACAGC ATATGTTCCC AAGGCCTGAG TTCTGGACCT ACCCCCACGT GGTGTAAGCA    900

GAGGAGGAAT TGGTTCACTT AACTCCCAGC AAACATCCTC CTGCCACTTA GGAGGAAACA    960

CCTCCCTATG GTACCATTTA TGTTTCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC   1020

CAGCAAATAG TTGGCACTCA ATAAAGATTT GCAGAATTTA ATACAGATCT TTTCAGCTGT   1080

TCTTAGGGCA TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA   1140

TGTGGAGCTA GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGAAG   1200

TCGCAGCAGA GAGGGACCAT CCAAATACCT AAGAGAAAAC AGACCTAGTC AGGATATGAA   1260

TTTGTTTCAG CTGTTCCCAA AGGCCTGGGA GCTTTTTGAA AAGAAAGAAA AAAGTGTGTT   1320

GGCTTTTTTT TTTTTTAGAA AGTTAGAATT GTTTTTACCA AGAGTCTATG TGGGGCTTGA   1380

TTCACCCTTC ATCCATTGGC TGGAACATGG ATTGGGGATT TGATAGAAAA ATAAACCCTG   1440

CTTTTGATTC AAAAAAAAAA AAAAAAWAAA AAAAACTCGA                         1480
```

(2) INFORMATION FOR SEQ ID NO: 208:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 872 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```
CAGTATTTCC CTCAGTACTG TAAGCAAAAG TGGTATGTTT TTCTTTCTTT ATGTCTACTC     60
```

```
     TGTCCTCTGT GGCCTTCTGG TGTACCCCTC TCTTCCTAGC CATTCAGTCT CTCTAGTCAC    120

     CTCCCTAGTA GCTAGTGCTC TCTAAGTTTT TATTTAATTA GAACAACTCC ATTTCCATTT    180

  5  CAAGGTAGGT CAATGGGGGG AAAAGCCTCA TGATTTAAAC TGAAGTTAAC AACACAGCTT    240

     TTAAAATGAA AACTCATACT CCAACTTCTA AAGTATATTT GAGCTGATTT GTTTCCAAAA    300

     CAAAGATATG CTGTACCTAA AACTGCTAAA ACAAAAATAT AAAGACAAGG ACTAGGTGAT    360

 10  TAAGGGGAGA GAAAAATCAT YTCTTTTCCA GGAAACCTTT GCTAAAATAA GCAAAACTTG    420

     ANTCTATGCT TCATGGAAAC TGACACAAAG AAAAGAAACT GATGGATTGC ACAGGCCTTG    480

 15  TTATAGAAAT AGATCTATAA AAAGATCTGT CCACAGGAAA TATACACCTT CTCCTGGTTC    540

     TGAACTTCAA TGGGGATTTG TCACCTAGGT CTCCATCTAT AGGAATACCT TCACATACCT    600

     ATCTATTCAT GCACATATTC TGAAAACAGG TACATACAAA ATTACAACAA AGGAAAAAAA    660

 20  TTCTATTGAA CACTTAAAAA TAGAAACAGG CCAGGCACGG TGGCTCATGC TGTAATCCCA    720

     ACAATTTGGG AGGCTGAGGC TGGTGGATCA CCTGAGGTCA GGAGTGTGAG ACCAGCTTGG    780

 25  CCAACATGGT GAAACCCCGT CACTACTAAA AATACAAAAA AAATTAGCCT GTGTGGTGGC    840

     ACACTCNTAC AATCCNGGCT GACTCGGGAA AN                                   872
```

 30

```
     (2) INFORMATION FOR SEQ ID NO: 209:

 35          (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1779 base pairs
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

 40          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

     AATTGCCAAG ACTGCACAAA ATTACAGTGC TAATGTATAT GGTTGCAGTT CACATAAAGA     60

     CAAAAGCATC TGTTATGAAA TGAGTAGTAA TATTGGGTGG TTGATTTGTT CTTAGCAGAC    120

 45  TTGGCTTCAT WTTGGTCTTG AGATAAAATG GCCAGCATAA ATGCTGTTTA TATTCACGTT    180

     TTCCTAGGTG TGTGTGTGCA GGCCACAGCA GCATGCCCTT GGTGTAGTCA GTGCCGAAAS    240

 50  GGGTCTGTTC CTTCTTGAGC CTGCCTGCAG GGATGGTCTC CTTTTAAAGC AGGTTGTGTG    300

     CAGCATTCAG TACACTGAAG GTAAGCTAAA CCATCAACAT CTCTGGTGTT TTAAGATGTT    360

     ATTTTATTGG AACAACTGAC AAATGAGGGA TGTTAGCTTT GTGGCAGAAT TCCCTGCATG    420

 55  TGTGATAACT GATCTTGTTT TATTTTTTGG CATTGCAACT GTGGCATAGT TACAATTTCT    480

     GTTTGKTCAT CACATTTAAA ATTGGRAGAG AACGCGCTTG AKGGATAGAG CGCCTTCAGK    540

 60  GTACTGTTTC TTATTAACTT TACTTTTTTT AAATCAACTT GCTATAGACT TTATATACAT    600
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462

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TTTGTTAAAT ATAGTTCCTA GTGACATAGA AACGATGCGT AGTTTTCATT TACTAATTAC          660

AAATGTTGAG GCCTAATTCT GAAAGTCCTC ATATTTAAAG GCTAGACAAC GTAATGAAAT          720

TTTTAACTAT TTGTATGTCA TTTTGAAAGT GTACTGCTTT ATGGTAAAAG TGTTTTTCAT          780

TTGTTCATTG TTTTCATTAT TTGTGATCAT GTTGTCTTTC AATACAGGCA TAAACCTTCC          840

ACTCTTGAAC AAAGCAGCTG CTTTTTAAAA GCGGTAATTG CTTCTTTACC TTTTATTTCT          900

TTTGTAAATG AAGCTTTTCT TTAAGAATGT GACTTTAAAG TGTTGTCTAT TGCATAAAAC          960

AGTTGACACT CACTTATTGT AAAGTGAAGA TTGTTCTACT GCATGTGAAG TGGACCATGC         1020

AGATTTCTGT ATGTTCTCAG TATGCATCAC TAGATAATAA AGTCTTTTGT GAACAAGGCA         1080

TTTGTAGCCA TTTTTAAAAG TTTTTGTCTT CAGTGCTGGT AAGTCAGGTA AACCATAAAT         1140

AGTTAAAAGC AACCTTTTGT TTTTTTCCTG AAAGTTTTTA ATTGAAAGTA TTATTAGTTA         1200

AAGATGTAAA CCTAGCCAAA ATTACCAGTT TATTAATAAT TAGGATCCTA ATTATTTCAA         1260

AAAATCCTAC AAATATTGTC AGCTTTCAGT GTAGTGAGAT TATTCCTGTA GGTTATGGGG         1320

TATAATTCAG GATTTAACTA ATGTTTCTGC TATTTTCTCA CTTTTCCTTT TGATGGTGCG         1380

GAAAGAGAAA AAGGAAAACG GGGCACAGGC CATTCGACGC CTTCTCCAAG GGGTCTGATT         1440

TGCTGAGACA CCAGCTTCAC CTTCTTAACA AGGCACCTAA TTACAACAAG CATGCACATT         1500

TTGGTGCATT CAAGAATGGA AAATCAGAAT AGCAGCATTG ATTCTTCTGG TGCAGCTCAG         1560

TGGAAGATGA TGACAACCAG AAGACATGAG CTAAGGGTAA GGGACTGTTC TGAAGAACCT         1620

TTCCATTTAG TGATCAAGAT ATGGAAGCTG ATTTCTGAAA ATGCTCAGTG TGTACTCTAA         1680

TTATTTATGG TACCATTTGA ATTGTAACTT GCATTTTAGC AGTGCATGTT TCTAATTGAC         1740

TTACTGGGAA ACTGAATAAA ATATGCCTCT TATTATCAA                               1779
```

(2) INFORMATION FOR SEQ ID NO: 210:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2110 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GCGGCCGCTG CAGCCCGGAG CTGAGCTAGC CGTCCGAGCC GAGCCGTCCG AGCCGGGGAA          60

GCCGGCGCGT GCTGCCGCTC GTGGCGGCCA GAGGAGAGGA GAGGCAGCAG CATGGCGAGT         120

GTCCTGTCCC GACGCCTTGG AAAGCGGTCC CTCCTGGGAG CCCGGGTGTT GGGACCCAGT         180
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       GCCTCGGAGG GGCCTCGGCT GCCCCACCCT CGGAGCCACT GCTAGAAGGG GCCGCTCCCC          240

       AGCCTTTCAC CACCTCTGAT GACACCCCCT GCCAGGAGCA GCCCAAGGAA GTCCTTAAGG          300

5      CTCCCAGCAC CTCGGGCCTT CAGCAGGTGG CCTTTMAGCC TGGGCAGAAG GTTTATGTGT          360

       GGTACGGGGG TCAAGAGTGC ACAGGACTGG TGGWGCAGCA CAGCTGGATG GAGGGTCAGG          420

       TGACCGTCTG GCTGCTGGAG CAGAAGCTGC AGGTCTGCTG CAGGGTGGAG GAGGTGTGGC          480
10
       TGGCAGAGCT GCAGGGCCCC TGTCCCCAGG CACCACCCCT GGAGCCCGGA GCCCAGGCCC          540

       TGGCCTACAG GCCCGTCTCC AGGAACATCG ATGTCCCAAA GAGGAAGTCG GACGCATGGA          600

15     AATGGATGAG ATGATGGCGG CCATGGTGCT GACGTCCCTG TCCTGCAGCC CTGTTGTACA          660

       GAGTCCTCCC GGGACCGAGG CCAACTTCTC TGCTTCCCGT GCGGCCTGCG ACCCATGGAA          720

       GGAGAGTGGT GACATCTCGG ACAGCGGCAN CAGCACTACC AGCGGTCACT GGAGTGGGAG          780
20
       CAGTGGTGTC TCCACCCCCT CGCCCCCCCA CCCCCAGGCC AGCCCCAAGT ATTTGGGGGA          840

       TGCTTTTGGT TCTCCCCAAA CTGATCATGG CTTTGAGACC GATCCTGACC CTTTCCTGCT          900

25     GGACGAACCA GCTCCACGAA AAAGAAAGAA CTCTGTGAAG GTGATGTACA AGTGCCTGTG          960

       GCCAAACTGT GGCAAAGTTC TGCGCTCCAT TGTGGGCATC AAACGACACG TCAAAGCCCT         1020

       CCATCTGGGG GACACAGTGG ACTCTGATCA GTTCAAGCGG GAGGAGGATT CTACTACAC          1080
30
       AGAGGTGCAG CTGAAGGAGG AATCTGCTGC TGCTGCTGCT GCTGCTGCCG CAGACCCCCA         1140

       GTCCCTGGGA CTCCCACCTC CGAGCCAGCT CCCACCCCCA GCATGACTGG CCTGCCTCTG         1200

35     TCTGCTCTTC CACCACCTCT GCACAAAGCC CAGTCCTCCG GCCCAGAACA TCCTGGCCCG         1260

       GAGTCCTCCC TGCCCTCAGG GGCTCTCAGC AAGTCAGCTC CTGGGTCCTT CTGGCACATT         1320

       CAGGCAGATC ATGCATACCA GGCTCTGCCA TCCTTCCAGA TCCCAGTCTC ACCACACATC         1380
40
       TACACCAGTG TCAGCTGGGC TGCTGCCCCC TCCGCCGCCT GCTCTCTMTC TCCGGTCCGG         1440

       AGCCGGTCGC TAAGCTTCAG CGAAGCCCCA GCAGCCAGCA CCTGCGATGA AATCTCATCT         1500

45     GATCGTCACT TCTCCACCCC GGGCCCAGAG TGGTGCCAGG AAAGCCCGAG GGGAGGCTAA         1560

       GAAGTGCCGC AAGTGTATGG CATCGAGCAC CGGGACCAGT GGTGCACGGC CTGCCGGTGG         1620

       AAGAAGGCCT GCCAGCGCTT TCTGGACTGA GCTGTGCTGC AGGTTCTACT CTGTTCCTGG         1680
50
       CCCTGCCGGC AGCCACTGAC AAGAGGCCAG TGTGTCACCA GCCCTCAGCA GAAACCGAAA         1740

       GAGAAAGAAC GGAAACACGG AGTTTGGGCT CTGTTGGCTA AGGTGTAACA CTTAAAGCAA         1800

55     TTTTCTCCCA TTGTGCGAAC ATTTTATTTT TTAAAAAAAA GAAACAAAAA TATTTTTCCC         1860

       CCTAAAATAG GAGAGAGCCA AAACTGACCA AGGCTATTCA GCAGTGAACC AGTGACCAAA         1920

       GAATTAATTA CCCTCCGTTT CCCACATCCC CACTCTCTAG GGGATTAGCT TGTGCGTGTC         1980
60
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464

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AAAAGAAGGA ACAGCTCGTT CTGCTTCCTG CTGAGTCGGT GAATTCTTTG CTTTCTAAAC    2040

TCTTCCAGAA AGGACTGTGA GCAAGATGAA TTTACTTTTC TTAAAAAAAA AAAAAAAAAA    2100

AAAAACTCGA                                                         2110
```

(2) INFORMATION FOR SEQ ID NO: 211:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 938 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
GGCACAGGAA AAAAAGAAA AAAGAAAAAA GAAAAAAGTT TTTGTACCCA CAGATTAGCA     60

TTTTCTTGAT GTTTGAAAAA AGTTTAAGCT ATGTCCTAAT TTAAAAATGA GCACAAACTA   120

CTTAACAGAT GTCTGTTCCC TCTTCTCTTA CTTAAATTAT CTTTATTTTC ACCATCACCT   180

CCCAGTGCCG AACACCTGAN CTCTGTGTTT TGTGGTTGGA TCCTGGGTTG CCAAGTTCCT   240

ATTTGGTCAG TCCCTGGCCT GTGGGGCGGT CTCAGGAAGT GGCATGCTCT TCAMGRAGGA   300

TCGTTCATYT CCAGTATAAC CAWTTTGTTA ATAATAGTTG ATAATTCCCA GCTTTTACCA   360

GATGARTTTT GACTTATTTT TCCTCCTTTG ACCTGTTCAA AGCTAACATA TCTCGGTCAG   420

TTCGGAGAGG GTGGGGGATT TGAGAATGTG AGGAGGAGTG GGGTTAGAAT GGGTTTGCCT   480

ATCTGGGCAA GGAAAGAGTT CCTAGTCGAT TGGGCACAAT GACAAAATGA TTCCATGGAT   540

AGAATCGTCC CATGTTGCTG GAACACCTCA CGTGTTGTGA ACGCCTTAAA TTCCTGCCAT   600

CCCTTCTCTG ATTCCCCACC TCCCTGTAGT TTCCACAGGA TTTATCTCTC TGTACCCCCG   660

TCCTCCAACT CTACTCTGTC AGCCTCTCCT CCATCCCTTA CTTCCCTTCT AAATTCCAGG   720

AGATGACCTC ACTTTGCAAA GCAAATTGGA GCCACCAAAT TGTAGCTCTC CTCGGTGGAA   780

ACTGCATCTG TGCTCATCCC TGCACCTTCT TGCAGAAAGC CGCCCCCTCA GGCCAAGATG   840

AGTGCCTGGC CCCCATGGGA GACTCAGACA CTTTGACCCC TTGTGACTTC AGCATCTCCC   900

TCTTTAAAGA TTCTCTCCCA ACATTCAGTC GTGCTCGA                          938
```

(2) INFORMATION FOR SEQ ID NO: 212:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1551 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

465

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```
AGGCTGGACT AAGCATAGAG AACCAGGAGA GAAAGAAAGA TTTAAGAGAC TGAGTAATAT       60

TTTTTGACAG ATCATTTAAG AAACTGAGTA ATTTTTTTTT CTCCAAAAG GGCATGGGTT       120

TTTTTTTTGT TTTGTTTTTT CTCTATTTGG CACTTTCTAG GGATTGGTCT ATAAATTTTT    .  180

TGAAAGATCA TAGGATAAAT TTCTTTGTAG CAACTTCCTA TTTTAGTGTT TATGTTAGGG       240

GARCCCCARG TGTCCCTGCT GATACGCCAT TAGGGCCACT TCTCAGCCTC TGGCTACATC       300

ATAATGCTTT TTTTTCTATC TTGCCAAAGT TTCCMGAAAA TTKAKGTTTT CTAATTTTAA       360

AAAAATTGGT TGTGGAGATG GGATGGGACC TCTTTATAAG CCCTGAAAAT AAGTGATTTN       420

TTTTAAGTGC TATTCTGCTA TAAACCTGAT TCTCACTTTT TTCTGTAGAC AACAGTTTTT       480

TATAATATAT CTATTTTGTG TGGACATTAT TTCCTTTTAA CCAATACTGA AATTCCATAG       540

TGTAWACTTT CTCCACATTT TCTTTGATTA ATACTTYCTT AAAATAGACA CTTGGATTGG       600

CACCAGCTGT CACCAATAAA GCTGCCCTGA ACATTGTCAA TCAATCCTGT TAACCAATTT       660

GAGAATTTTT CTGGAATGCT TAGTTAGGGA TGAAATTGCT GGGTTATAGG TATGAGTATG       720

CTTGATATAC TTTTCTCCAG AATGTCTACA CCTGTGTGTA CACCACATCT CCAGAGATAG       780

GGGAATCTTA TGTCCCTGCT AACTGCTCTC GTTATTTAAT TTTCTGACAT TTGCCGCCGC       840

CGCCGCCCCC TGCCCCCAAC ACACACATGG TATAAAGTGG TAGTTTCTTG TTTTAAATTG       900

AACTTTTGAA TGATTTGAAT TTGGGCATTT CTTTGTATCC TGAGTTATTT TGGTTTCCCG       960

TTATGTGAAT ATCCTTTTCC TATGCTTTAA CTACTTTTCT AATTTGTCCC TTTTTTNGGT      1020

TATCAAATTC CAGGCCATTG TCTATTCCAT CGTCACTTTT GGGTATTGGA AACATCTTTC      1080

CATTCTGTAG CCTGTCTGTT GAACATAAAT CTTGATTTTT ATGTAATCAG ATTTTTCTCC      1140

TTACGGTTAT GTTCTTGGAA TTTTATTTAA GAAATCTTTT TCTATCCTGA GACCACAAAA      1200

ATGTCCCCAC CATTTTCTTC TGTTTCATAG TTTTGCCTTG TATGTTTAAT CCTTTAAGGC      1260

ATGTGTAGTT CATTTTATAT GGTGTGAAAT AGTTCTTATT CATTTATTCA ACACATATTG      1320

GTGGAGTGCC TGCTGATGGT AGTACTCTTC AGAGTACTTT GTATATATTT GTGAACACAT      1380

ATTCTTGCCC TGGAAGCTTA TGTTGTCNTT CAAGGTAGAT CCNTACTCGG TTTCCACCTG      1440

TTTTCTTCAG CCCTCAGGAT GAATTCCACA ATTTTACACA TAGCACCAGT TAAGGAATAG      1500

GCTTTATTGG AGAAAAGGAA GGCTTATTAG ACCAGCATCA GCAAAAAAAA A              1551
```

(2) INFORMATION FOR SEQ ID NO: 213:

466

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 997 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

AGAGAGTCCT CAACAGAACC TAATCATGCT GGCACCCTAA TCTCATACTT CTAGCCTCCA   60

GAACTGAGAG AACATAAACT CCAGTTGTTT AAGCTACCCA GACTATGGTA TTTGTTATTA   120

TAGCCCAAGC TAAGTCAGGT GGAAAGGCAG AAATATTTTG AGAAGATCA TTTCTACAAA   180

AACAGAGTTG TTCTAAATGA AATGGCCAGA TATTTCATCT TCTTCATACT AGTATTTATG   240

AAAGTTTCAT TAAACACCAC TTGGCCAGCA CCCAGGCCTG CTACCCTCAG AACGGCAAC   300

AAAAGCAAAT GATTTGAGGA ACAAAGAGT GGACACAGAG CTTCTCAGAA GATGGCTCA   360

TCTTCTGAGA TGATCTTCTG AGATCATCAA TTTTCTGCAC CTGATGTCCT ACTCCAATG   420

TAGTAGATAA GAGCAAAGAC ACTTCCTGAT CCTGTGGAAA ATGCTGGAGC CCTGCTGATG   480

GAGAGGCTGA CACTGGGACC AACAGAAGGC CGGACATTTA TTTGTTGCAG CCCTTCTGCA   540

CCTGGGCCCT CTTCAGGCCT TGTACCTTGC ACTCCCCATG CCACTGTAGC ACCTGGTAAG   600

CTGAAGTTAG GTATTTGAAG AGATAATTTG CCCCCAACAA AGAATTACTT AAAAGAAAA   660

GGAAACCACT AAATTCCACT TGACAAACCA GTTTGTTCAG TTTTGACTTT TGCAAATTTG   720

AAACTTTCTC TTTGGCACCA TATGATTCTG TTACATTAGG GTTCATCAAT GCTAAGATAC   780

ACAGCTAGGT CTACCAGCTG CCAGTGGTCA AGAATGAAAG AACCTCTCAG AGAGAGATCA   840

GTTTCTAATA ACCTAACAGT TTTCCTTGGS TATTACMAAA AAAAAAAAA TTAGAATAAA   900

ATGTCAGTGC CATGCAGGCA AGTACAGATA TGGAAATGAA AGCTTTGTCT ACAACTGCAA   960

GATTTGTTTG TTAATAAAAT TGATTGGGAT CACTCGA   997

(2) INFORMATION FOR SEQ ID NO: 214:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1496 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

GAATTCGGCA CGAGTGACCA CAGATATCTT TGGCTTTCAG CCTCCCCACA ATGCTGTCCA   60

CTATGTTTTT TTTAATCGAT TGACATCTCA TGAATCCACA AATTTAGCCG CTTTTCCATC   120

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TTTTCCATCT TTGTCATAGC TTCATCACGC ACGATGGAGG TCACTTCAGC ACTATCCGGA     180

GCGGCCTCAC GGACAGATCR GTGAATTTCC TTTTCCTTTT TCTTGATGTA CCGGATTGTC     240

GACTCGTTAA CATTGAGCTC ATGGCCAACA GCACTGTAAC TCATGCCTGA TTGGAGCTTA     300

TCCAACACGC GGAMTTTCTC CGTAAGGSAM ATCAMGGTCT TCTTTCGCTT AGGAACACTG     360

GGCARARCTT AARCACTACG CTTGGGGGCC ATTTTAGAAA GCAAAACCAC CCACAAAAAG    420

CAGAAAAAAA AGTGTCAGTA AACAGACTGN NGANAGGACT CTTTGTTTAC AGCACAGGAG     480

CTGCGACTAG AAGGCGGCGC TTCTCCCCAG TTCAAACTTC AGCTGGGAAC CTTACCTCCG     540

CCAACTCCAA ATTTTCACCC TCTGCGCATG CCCGGGAAAS AAACCCCCAG AACAGTACCG     600

TGATGATTGA TTTTAGGGTT ACAAATACAT TTTAGCAAGT AAGTGAATTT GGCATTACGA     660

ATTAATGATT AATGAAGGTC ACCTGTATTT CCATAGATAT GTAATTTTAT TTAAGCAGGT     720

TTATTATATT AAGGCGGSGA GGCAGCGCCG AAGACTACAA GTTCCAGCAT GCACCGCGTC     780

CGGGCGGGTT CGGGCTCCCA GCGAGGGCTT CAGGGACGCC AGCCCGGAGG CATCGGCCGG     840

AAGTGTCGTA GGGCAACCAC GTAGTACTCT CTGCGCATGT GCAAAGCGCT GTCGGGGGCC     900

GCCCTAGCTG CCGTCGCCGC CGCCGGGGCT CTATGGTCTC TCCCTAGAGC TTTGCCGTTG     960

GAGGCGGCTG CTGCGGTCTT GTGAGTTTGA CCAGCGTCGA GCGGCAGCAA CATGGAGGAA    1020

TTCGACTCCG AAGACTTCTC TACGTCGGAG GAGGACGAGG ACTACGTGCC GTCGGGTGAG    1080

CGATTCCGCC TGAGGCGAGA AGCGAATTGC CCCGCCCCAC GCCTCACGTG AGGCGCGCTC    1140

TGCCCCCGCG GGCGTCTGCC CTGTGGCCCA GGTGGTCCAG GGGGGCTCCT GTTCTCGAGC    1200

GTCCGCTCCC TCAGGCCCCT CATCCTCGGC CGCTCCGGCC CGAGGCGTGT GCGCGTGGCG    1260

GTTCTGTGCT CCCCTCCCGT TGGGCAGCTC CGGCCGCCGC CCCCTCTTGC AGCGCGGGAA    1320

CGGCACATGG ACACGGCCCC TTGTCGCTAG GGACGCTCGT CGGTCAGCCC CGAACGACAA    1380

CGCTGCTTCA GAAGTCGGGG CGGCAGTTCG AGCCTTGGAA GTTTTTTTCA GCCCTGGCCC    1440

GAGAGAGCTG CTGGCCAACA ACCCGTCCAA GATAGAGCTG TCCGNTCTCC GNCTGG        1496
```

(2) INFORMATION FOR SEQ ID NO: 215:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1308 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

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TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC      60
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CTGCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA        120

AAAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG        180

TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA        240

ACACAAACAC TGTCCTTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC        300

GTATTCCACG TTTTTAGCCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT        360

TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG        420

AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA        480

AAAAGCCAGG TATAATGTAA CTTCACCCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA        540

TACTCTTTTA AGTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC        600

CATTTTTACT ATTAAGAAGA CCAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT        660

AAGTGAGAGT GTGAACTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC        720

AGGCCTTATG TTAAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAAA GACAGCAGCA        780

AGCATTATAC GGTCATCTTG AATGATCCCT TTGAAATTTT TTTTTTGTTT GTTTGTTTAA        840

ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTC TGTGAATGCT        900

AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC        960

TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAAACT GTTTACATTC ATTATGGGGT       1020

ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA       1080

ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAACTC AGAGACAGCA CTGCCTTCTC       1140

CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA       1200

GCCATAACCC TTTTTTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCGGTATA       1260

TAATACTGGT WCCAACAMAG GGGTTCTGGA TGTACACMAG GTTATCTT                    1308
```

(2) INFORMATION FOR SEQ ID NO: 216:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1705 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```
TGGCCATGGA AGCGCTAGAA GGTTTAGATT TTGAAACAGC AAAGAAGGAT TTCCTTGGAT         60

CTGGAGACCC CAAAGAAACA AAGATGCTAA TCACCAAACA GGCTGACTGG GCCAGAAATA        120
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      TCAAGGAGCC CAAAGCCGCC GTGGAGATGT ACATCTCAGC AGGAGAGCAC GTCAAGGCCA        180

      TCGAGATCTG TGGTGACCAT GGCTGGGTTG ACATGTTGAT CGACATCGCC CGCAAACTGG        240

  5   ACAAGGCTGA GCGCGAGCCC CTGCTGCTGT GCGCTACCTA CCTCAAGAAG CTGGACAGCC        300

      CTGGCTATGC TGCTGAGACC TACCTGAAGA TGGGTGACCT CAAGTCCCTG GTGCAGCTGC        360

      AGTGGAGACC CAGCGCTGGG ATGAGGCCTT TGCTTTGGGT GAGAAGCATC CTGAGTTTAA        420

 10   GGATGACATC TACATGCCGT ATGCTCAGTG GCTAGCAGAG AACGATCGCT TTGAGGAAGC        480

      CCAGAAAGCG TTCCACAAGG CTGGGCGACA GAGAGAAGCG GTCCAGGTGC TGGAGCAGCT        540

 15   CACAAACAAT GCCGTGGCGG AGAGCAGGTT TAATGATGCT GCCTATTATT ACTGGATGCT        600

      GTCCATGCAG TGCCTCGATA TAGCTCAAGA TCCTGCCCAG AAGGACACAA TGCTTGGCAA        660

      GTTCTACCAC TTCCAGCGTT TGGCAGAGCT GTACCATGGT TACCATGCCA TCCATCGCCA        720

 20   CACGGAAGAT CCGTTCAGTG TCCATCGTCC TGAAACTCTT TTCAACATCT CCAGGTTCCT        780

      GCTGCACAGC CTGCCCAAGG ACACCCCCTC GGGCATCTCT AAAGTGAAAA TACTCTTCAC        840

 25   CTTGGCCAAG CAGAGCAAGG CCCTCGGTGC CTACAGGCTG GCCCGGCACG CCTATGACAA        900

      GCTGCGTGGC CTGTACATCC CTGCCAGATT CCAAAAGTCC ATTGAGCTGG GTACCCTGAC        960

      CATCCGCGCC AAGCCCTTCC ACGACAGTGA GGAGTTGGTG CCCTTGTGCT ACCGCTGCTC       1020

 30   CACCAACAAC CCGCTGCTCA ACAACCTGGG CAACGTCTGC ATCAACTGCC GCCAGCCCTT       1080

      CATCTTCTCC GCCTCTTCCT ACGACGTGCT ACACCTGGTT GAGTTCTACC TGGAGGAAGG       1140

 35   GATCACTGAT GAAGAAGCCA TCTCCCTCAT CGACCTGGAG GTGCTGAGAC CCAAGCGGGA       1200

      TGACAGACAG CTAGAGATTT GCAAACAACA GCTCCCAGAT TCTTGCGGCT AGTGGGAGAC       1260

      CAAGGGACTC CATCGGAGAT NAGGACCCGT TCACAGCTAA GCTRAGCTTT GAGCAAGGTG       1320

 40   GCTCARAGTT CGTGCCAGTG GTGGTGAGCC GGCTGGTGCT GCGCTCCATG AGCCGCCGGG       1380

      ATGTCCTCAT CAAGCGATGG CCCCCACCCC TGAGGTGGCA ATACTTCCGC TCACTGCTGC       1440

 45   CTGACGCCTC CATTACCATG TGCCCCTCCT GCTTCCAGAT GTTCCATTCT GAGGACTATG       1500

      AGTTGCTGGT GCTTCAGCAT GGCTGCTGCC CCTACTGCCG CAGGTGCAAG GATGACCCTG       1560

      GCCCATGACC AGCATCCTGG GGACGGCCTG CACCCTCTGC CCGCCTTGGG GTCTGCTGGG       1620

 50   CTGTGAAGGA GAATAAAGAG TTAAACTGTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA       1680

      AAAAAAAAAA AAAAAAAAAA AAANA                                           1705
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 55

      (2) INFORMATION FOR SEQ ID NO: 217:

 60   (i) SEQUENCE CHARACTERISTICS:

470

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          (A) LENGTH: 999 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGCAAATCAC CTTAACGATC TGGAATGAAA CTGTGACCAG TGCCGCCCTG GGTGGTTCTG      60

GAGAGACTGC CGTCTTCTTG TTTGGCCATA GGTGCTGGGG CCCCGGCTTC AGTCACTGTC     120

TCAGACAGKA GTCCCGATAA GCAGATCACC AGTCCTCCAC TGTCCTTCCT GTCGGCCTTG     180

CTGCATGAGA AGATAGCTGC TTCCTCCCTC TTTTCCTACA CTGTAAATTA TTGTTTTACA     240

ATTGAGTGYC TTAATAATAG TYTACAAATA CTATGTATTT ATGCAAAACT GTTAAAGTTC     300

TCATCTGTTA TGATTGGATA CTTGGTCTTG TCAGTAGTGG TCAGCATTGG GTTGTGAGCT     360

TGTCCTACTC CATACGTGTT TATCCTGCTA TGCATTTTAC ATTGTGTGTT CACATCTATT     420

CCAAGGAGCC TTGCTAGAAA CAACACTGGC GGTTCCTGCA GGCCAGGCAG GCATTGGCCC     480

ATGCTGTGTC CCATAGGAGC CAATGGAAAG AACGTAGCTT GGTCTGCTAG CCAGCCGTGG     540

GGTGGCGCAG GCCAGGCAGC CTCTGCACCA GAGTCCAGCA CCTGCCCATT CCCCAGTCAC     600

ACAATCATAC TCTTCTTTCA TAGAGATTTT ATTACCACCT AGACCACCCT AGTTTTCCTC     660

TCTGTTAGTG TCCTGAGCTC TTTTGCAACA AAATGTAGGT ACAGACCAAT CCCTGTCCCT     720

TCCCCAATCA GGAGCTCCAC ACCATGAGTT GTTTGGTTTT CCAGAAGCTG CCAGTGGGTT     780

CCCGTGAATT GCGTTAAGAT ATCGATGATK TTTTTTATTG TTTTTCTTCT TGTTTTTTTA     840

AATAATATAT TTAAAGGCAG TATCTTTTGT ACTGTGAATT TGCAGTAGAA GATGCAGAAT     900

GCACTTTTTT TTTACTTCTG TTGGTGTGTA TTGTATATAG TGTGTGTGCT TCTTGTGATG     960

AAAATAAACT TTTTCTTTAT AAAAAAAAAA AAAAAAAC                             999
```

(2) INFORMATION FOR SEQ ID NO: 218:

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      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 941 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGCACGAGTA GCATTTCATT TAATCTGCAG GTATATTCTC CCAACAGTTT ATTGTCATGT      60

GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA     120

GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA     180
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60

471

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    TGTCCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA      240

    GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT      300

 5  TCTGCTCTTC TTTTTTCTCC CCCTTATATT GTGCTTTCAT TCATTCATTC ATTCATCAAA      360

    CATTTGTTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC      420

    ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA      480

10  GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC      540

    GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC      600

15  TGAAGGTGGC AGTGCCTGGA GTCTTGATTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC      660

    ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTTCTG GATGGCSCTG      720

    GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACTTCCA      780

20  TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTTAA GGCTGGTCCG      840

    AGTAGAATGA TTTTTACAAC GAATTGATCA CAACCAGTTA CAGATGTCTT TGTTCCTTCT      900

25  CCACTCCCAC TGCTTCACCT GACTAGCCTT TAAAAAAAAA A                          941
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40  TAAGTGGAAT CCCCCGGGGT TGCAGGGAAT TCGGCACGAG GCATTCTGAG AAGCTTAAGA       60

    CATACTTTGA AGACAACCCT AGGGACCTCC AGCTGCTGCG GCATGACCTA CCTTTGCACC      120

    CCGCAGTGGT GAAGCCCCAC CTGGGCCATG TTCCTGACTA CCTGGTTCCT CCTGCTCTCC      180

45  GTGGCCTGGT RCGCCCTCAC AAGAAGCGGA AGAAGCTGTC TTCCTCTTGT AGGAAGGCCA      240

    AGAGAGCAAA GTCCCAGAAC CCACTGCGCA GCTTCAAGCA CAAAGGAAAG AAATTCAGAC      300

50  CCACAGCCAA GCCCTCCTGA GGTTGTTGGG CCTCTCTGGA GCTGAGCACA TTGTGGAGCA      360

    CAGGCTTACA CCCTTCGTGG ACAGGCGAGG CTCTGGTGCT TACTGCACAG CCTGAACAGA      420

    CAGTTCTGGG GCCGGCAGTG CTGGGCCCTT TAGCTCCTTG GCACTTCCAA GCTGGCATCT      480

55  TGCCCCTTGA CAACAGAATA AAAATTTTAG CTGCCCCAAA AAAAAAAAAA AAAAAAAAA       540

    CTCGAGGGGG GGCCCGTACC CAATTCGCCC TATAA                                 575
```

60

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(2) INFORMATION FOR SEQ ID NO: 220:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3018 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```
GCCAGCCTTA CAGGTTTTAC GTGAAATGAA AGCCATTGGA ATAGAACCCT CGCTTGCAAC          60

ATATCACCAT ATTATTCGCC TGTTTGATCA ACCTGGAGAC CCTTTAAAGA GATCATCCTT         120

CATCATTTAT GATATAATGA ATGAATTAAT GGGAAAGAGA TTTTCTCCAA AGGACCCGGA         180

TGATGATAAG TTTTTTCAGT CAGCCATGAG CATATGCTCA TCTCTCAGAG ATCTAGAACT         240

TGCCTACCAA GTACATGGCC TTTTAAAAAC CGGAGACAAC TGGAAATTCA TTGGACCTGA         300

TCAACATCGT AATTTCTATT ATTCCAAGTT CTTCGATTTG ATTTGTCTAA TGGAACAAAT         360

TGATGTTACC TTGAAGTGGT ATGAGGACCT GATACCTTCA GCCTACTTTC CCCACTCCCA         420

AACAATGATA CATCTTCTCC AAGCATTGGA TGTGGCCAAT CGGCTAGAAG TGATTCCTAA         480

AATTTGGGAA AGATAGTAAA GAATATGGTC ATACTTTCCG CAGTGACCTG AGAGAAGAGA         540

TCCTGATGCT CATGGCAAGG GACAAGCACC CACCAGAGCT TCAGGTGGCA TTTGCTGACT         600

GTGCTGCTGA TATCAAATCT GCGTATGAAA GCCAACCCAT CAGACAGACT GCTCAGGATT         660

GGCCAGCCAC CTCTCTCAAC TGTATAGCTA TCCTCTTTTT AAGGGCTGGG AGAACTCAGG         720

AAGCCTGGAA AATGTTGGGG CTTTTCAGGA AGCATAATAA GATTCCTAGA AGTGAGTTGC         780

TGAATGAGCT TATGGACAGT GCAAAAGTGT CTAACAGCCC TTCCCAGGCC ATTGAAGTAG         840

TAGAGCTGGC AAGTGCCTTC AGCTTACCTA TTTGTGAGGG CCTCACCCAG AGAGTAATGA         900

GTGATTTTGC AATCAACCAG GAACAAAAGG AAGCCCTAAG TAATCTAACT GCATTGACCA         960

GTGACAGTGA TACTGACAGC AGCAGTGACA GCGACAGTGA CACCAGTGAA GGCAAATGAA        1020

AGTGGAGATT CAGGAGCAGC AATGGTCTCA CCATAGCTGC TGGAATCACA CCTGAGAACT        1080

GAGATATACC AATATTTAAC ATTGTTACAA AGAAGAAAG ATACAGATTT GGTGAATTTG        1140

TTACTGTGAG GTACAGTCAG TACACAGCTG ACTTATGTAG ATTTAAGCTG CTAATATGCT        1200

ACTTAACCAT CTATTAATGC ACCATTAAAG GCTTAGCATT TAAGTAGCAA CATTGCGGTT        1260

TTCAGACACA TGGTGAGGTC CATGGCTCTT GTCATCAGGA TAAGCCTGCA CACCTAGAGT        1320

GTCGGTGAGC TGACCTCACG ATGCTGTCCT CGTGCGATTG CCCTCTCCTG CTGCTGGACT        1380

TCTGCCTTTG TTGGCCTGAT GTGCTGCTGT GATGCTGGTC CTTCATCTTA GGTGTTCATG        1440
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CAGTTCTAAC ACAGTTGGGG TTGGGTCAAT AGTTTCCCAA TTTCAGGATA TTTCGATGTC        1500

AGAAATAACG CATCTTAGGA ATGACTAAAC AAGATAATGG CAGTTTAGGC TGCACAACTG        1560

GTAAAATGAC TGTAGATAAA TGTTGTAATT AGTGTACACG TTTGTATTTT TGTTAATATA        1620

GCCGCTGCCA TAGTTTTCTA ACTTGAACAG CCATGAATGT TTCATGTCTC CCTTTTTTTT        1680

TTGTCTATAG CTGTTACCTA TTTTAGTGGT TGAAATGAGA GCTAGTGATG ACAGAAGGAT  .     1740

GTGGAATGTC TTCTTGACAT CATTGTGTAT TGCTGGTAAT CAAGTTGGTA ACGACTACTT        1800

CTAGCAGCTC TTACCACTAT GACTTAAGTG GTCCTGGAAG GCAGTAAGTG GAGGTTTGCA        1860

GCATTCCTGC CTTCATGAGG GCTTCTACCA CTGACCACTT TGCACGTACC TGGCTCCCAG        1920

ATTTACTTAG GTACCCCACG AGTCGTCCAC ATAAGCAGCT TCATCTTTAC CTTGCCAGAG        1980

TTGACAATTA TGGGATACTC TAGTCTACTT ATACTTGTGT TCCCATCTGT CTGCCATCCT        2040

CTGAAGGCCA GGACCCAGTC ATACATCCTT AGAAACCAAA GTATGGTTTT TGTTTTCTCT        2100

TGGAATGTCA GGTCTTAAGG CATTTAATTG AGGGACAAAA AAAAAAAAAA GCCGATATAG        2160

TAGCTAGCTA CTTAAGCATC CATGGGTATT GCTCCATATC AAAGCAGATT TGCAGGACAG        2220

AAAGAGTAAA TTAGCCTTCA GTCTTGGTTT ACAGCTTCCA AGGAGAGCCT TGGSCACCTG        2280

AAATGTTAAC TCGGTCCCTT CCTGTCTCTA GTTCATCAGC ACCTGCAGAT GCCTGACTCT        2340

TGTTAGCCTT ACTATTCAAT ACAGTCCTTA GATTCACGGT ATGCCTCTTC CTATCCAGGC        2400

ACCTATTCTG AATCACCATG TTGCTCTGCA GCTAGAGTTG ATAGGAGAAA ATCCATTTGG        2460

GTAGATGGCC TATGAATTTG TAGTAGACTT TCAAAATGAG TGATTTGTTA GCTTGGTACT        2520

TTTAAGTTTG TGGTACAGAT CCTCCAAACC CATACTCTGA GCAATTAACT GCCTTGAACA        2580

TAGAGAAAAA TTAAGGCCTC ACAGGATGAG TCTCCATTCT CTGTAAATGC TTATTTTATC        2640

ATAGTCTTTA GCCTCTAACT ATGAGTAAAA TGTTCTCTTC GGCCGGGTGT GGTGACTCAC        2700

ACCTGTAACC TCAGCACTTT GGGAGGCAGA GGTGGGAGGA TCACTTAGGT CCAGGAGTTC        2760

GAGACTAGCC TGGGCAACAT AGTGAGACAC CGGATCTACA AAAAAATAAA AAGCCAGACT        2820

GGTGGTATGT ATCTGTGTCC CAGCTAATTG GGAGGGTGAG ATGGGAGGAT TGTTTGAGCC        2880

TAGGAGAGGG AGGTTGCAGT GAGCCGTGAT CGCACCACTG CACTCCAGCC TGGGCAACAG        2940

AGCAAGACCC TGTCTTGGAG AAACCAGAAT TTTGGAAGAG CAAATGGGGC TGAGTGCAGT        3000

GGCTCATGCC TGTAATCC                                                     3018
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(2) INFORMATION FOR SEQ ID NO: 221:

        (i) SEQUENCE CHARACTERISTICS:

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```
         (A) LENGTH: 968 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GGCACGAGGG CCGCGGGACA TCCACGGGGC GCGAGTGACA CGCGGGAGGG AGAGCAGTGT      60

TCTGCTGGAG CCGATGCCAA AAACCATGCA TTTCTTATTC AGATTCATTG TTTTCTTTTA     120

TCTGTGGGGC CTTTTTACTG CTCAGAGACA AAAGAAAGAG GAGAGCACCG AAGAAGTGAA     180

AATAGAAGTT TTGCATCGTC CAGAAAACTG CTCTAAGACA AGCAAGAAGG GAGACCTACT     240

NAAATGCCCA TTATGACGGC TACCTGGCTA AAGACGGCTC GAAATTCTAC TGCAGCCGGA     300

CACAAAATGA AGGCCACCCC AAATGGTTTG TTCTTGGTGT TGGGCAAGTC ATAAAAGGCC     360

TAGACATTGC TATGACAGAT ATGTGCCCTG GAGAAAAGCG AAAAGTAGTT ATACCCCCTT     420

CATTTGCATA CGGAAAGGAA GGCTATGCAG AAGGCAAGAT TCCACCGGAT GCTACATTGA     480

TTTTTGAGAT TGAACTTTAT GCTGTGACCA AAGGACCACG GAGCATTGAG ACATTTAAAC     540

AAATAGACAT GGACAATGAC AGGCAGCTCT CTAAAGCCGA GATAAACCTC TACTTGCAAA     600

GGGAATTTGA AAAAGATGAG AAGCCACGTG ACAAGTCATA TCAGGATGCA GTTTTAGAAG     660

ATATTTTTAA GAAGAATGAC CATGATGGTG ATGGCTTCAT TTCTCCCAAG GAATACAATG     720

TATACCAACA CGATGAACTA TAGCATATTT GTATTCTAC TTTTTTTTTT TAGCTATTTA      780

CTGTACTTTA TGTATWAAAC AAAGTCMCTT TTCTCCMAGT TGKATTTGCT ATTTTTCCCC     840

TATGAGAAGA TATTTTGATC TCCCCAATAC ATTGATTTTG GTATAATAAA TGTGAGGCTG     900

TTTTGCAAAC TTAAAAAAAA ATTTAAAAAA ACTGGAGGGG GGCCCGTACC CAANTCGCCG     960

NATATGAT                                                            968
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(2) INFORMATION FOR SEQ ID NO: 222:

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         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1404 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CGTTTTCCGG CCGTGCGTTT GTGGCCGTCC GGCCTCCCTG ACATGCAGCC CTCTGGACCC      60

CGAGGTTGGA CCCTACTGTG ACACACCTAC CATGCGGACA CTCTTCAACC TCCTCTGGCT     120

TGCCCTGGCC TGCAGCCCTG TTCACACTAC CCTGTCAAAG TCAGATGCCA AAAAAGCCGC     180
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CTCAAAGACG CTGCTGGAGA AGAGTCAGTT TTCAGATAAG CCGGTGCAAG ACCGGGGTTT          240

GGTGGTGACG GACCTCAAAG CTGAGAGTGT GGTTCTTGAG CATCGCAGCT ACTGCTCGGC          300

AAAGGCCCGG GACAGACACT TTGCTGGGGA TGTACTGGGC TATGTCACTC CATGGAACAG          360

CCATGGCTAC GATGTCACCA AGGTCTTTGG GAGCAAGTTC ACACAGATCT CACCCGTCTG          420

GCTGCAGCTG AAGAGACGTG GCCGTGAGAT GTTTGAGGTC ACGGGCCTCC ACGACGTGGA       .  480

CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA TGCCAAGGGC CTGCACATAG TGCCTCGGCT          540

CCTGTTTGAG GACTGGACTT ACGATGATTT CCGGAACGTC TTAGACAGTG AGGATGAGAT          600

AGAGGAGCTG AGCAAGACCG TGGTCCAGGT GGCAAAGAAC CAGCATTTCG ATGGCTTCGT          660

GGTGGAGGTC TGGAACCAGC TGCTAAGCCA GAAGCGCGTG GGCCTCATCC ACATGCTCAC          720

CCACTTGGCC GAGGCTCTGC ACCAGGCCCG GCTGCTGGCC CTCCTGGTCA TCCCGCCTGC          780

CATCACCCCC GGGACCGACC AGCTGGGCAT GTTCACGCAC AAGGAGTTTG AGCAGCTGGC          840

CCCCGTGCTG GATGGTTTCA GCCTCATGAC CTACGACTAC TCTACAGCGC ATCAGCCTGG          900

CCCTAATGCA CCCCTGTCCT GGGTTCGAGC CTGCGTCCAG GTCCTGGACC CGAAGTCCAA          960

GTGGCGAAGC AAAATCCTCC TGGGGCTCAA CTTCTATGGT ATGGACTACG CGACCTCCAA         1020

GGATGCCCGT GAGCCTGTTG TCGGGGCCAG GTACATCCAG ACACTGAAGG ACCACAGGCC         1080

CCGGATGGTG TGGGACAGCC AGGYCTCAGA GCACTTCTTC GAGTACAAGA AGAGCCGCAG         1140

TGGGAGGCAC GTCGTCTTCT ACCCAACCCT GAAGTCCCTG CAGGTGCGGC TGGAGCTGGC         1200

CCGGGAGCTG GGCGTTGGGG TCTCTATCTG GGAGCTGGCC AGGGCCTGGA CTACTTCTAC         1260

GACCTGCTCT AGGTGGGCAT TGCGGCCTCC GCGGTGGACG TGTTCTTTTC TAAGCCATGG         1320

AGTGAGTGAG CAGGTGTGAA ATACAGGCCT NCACTCCGTT TGCTGTGAAA AAAAAAAAAA         1380

AAAAAAAAAA AAAAAAAAAA AAAA                                                1404
```

(2) INFORMATION FOR SEQ ID NO: 223:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 707 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

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NGCGCGCCTG CAGTCGACAC TAGTGGATCC AAAGAATTCG GCACGAGGGC AGGTCCAGGG           60

CTCAGAAATC AGCTCTATTG ACGAATTCTG CCGCAAGTTC CGCCTGGACT GCCCGCTGGC          120

CATGGAGCGG ATCAAGGAGG ACCGGCCCAT CACCATCAAG GACGACAAGG CAACCTCAA          180
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CCGCTGCATC GCAGACGTGG TCTCGCTCTT CATCACGGTC ATGGACAAGC TGCGCCTGGA   240

GATCCGCGCC ATGGATGAGA TCCAGCCCGA CCTGCGAGAG CTGATGGAGA CCATGCACCG   300

CATGAGCCAC CTCCCACCCG ACTTTGAGGG CCGCCAGACG GTCAGCCACT GGCTGCAGAC   360

CCTGAGCGGC ATGTCGGCGT CAGATGAGCT GGACGACTCA CAGGTGCGTC AGATGCTGTT   420

CGACCTGGAG TCAGCCTACA ACGCCTTCAA CCGCTTCCTG CATGCCTGAG CCCGGGGCAC   480

TAGCCCTTGC ACAGAAGGGC AGAGTCTGAG GCCATGGCTC CTGGTCCCCT GTCCGCCACA   540

CAGGCCGTGG TCATCCACAC AACTCACTGT CTGCAGCTGC CTGTCTGGTG TCTGTCTTTG   600

GTGTCAGAAC TTTTGGGCCG GGCCCCTCCC CACAATAAAG ATGCTCTCCG ACCTTCAAAA   660

AAAAAAAAAA AAAAACTCRG GGGGGCCCCG GTCCCAATCC CCCCNTTN   707

(2) INFORMATION FOR SEQ ID NO: 224:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1384 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGGGAACTGC AGTGACAGCA GGAGTAAGAG TGGGAGGCAG GACAGAGCTG GGACACAGGT   60

ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGGTGCCG GCGGTGAGAA   120

TCCAGGGAGA GGAGCGGAAA CAGAAGAGGG GCAGAAGACC GGGGCACTTG TGGGTTGCAG   180

AGCCCCTCAG CCATGTTGGG AGCCAAGCCA CACTGGCTAC CAGGTCCCCT ACACAGTCCC   240

GGGCTGCCCT TGGTTCTGGT GCTTCTGGCC CTGGGGGCCG GGTGGGCCCA GGAGGGGTCA   300

GAGCCCGTCC TGCTGGAGGG GGAGTGCCTG GTGGTCTGTG AGCCTGGCCG AGTTGCTGCA   360

GGGGGGCCCG GGGGAGCAGC CCTGGGAGAG GCACCCCCTG GGCGAGTGGC ATTGCTGCG   420

GTCCGAAGCC AMCACCATGA GCCAGCAGGG GAAACCGGCA ATGGCACCAK TGGGGCCATC   480

TACTTCGACC AGGTCCTGGT GAACGAGGGC GGTGGCTTTG ACCGGGCCTC TGGCTCCTTC   540

GTAGCCCCTG TCCGGGGTGT CTACAGCTTC CGGTTCCATG TGGTGAAGGT GTACAACCGC   600

CAAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCCTG TCATCTGCGC CTTTGCCAAT   660

GATCCTGACG TGACCCGGGA GGCAGCCACC AGCTCTGTGC TACTGCCCTT GGACCCTGGG   720

GACCGAGTGT CTCTGCGCCT GCGTCGGGGG AATCTACTGG GTGGTTGGAA ATACTCAAGT   780

TTCTCTGGCT TCCTCATCTT CCCTCTCTGA GGACCCAAGT YTTTCAAGCA CAAGAATCCA   840

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GCCCCTGACA ACTTTCTTCT GCCCTCTCTT GCCCCAGAAA CAGCAGAGGC AGGAGAGAGA        900

CTCCCTCTGG YTCCTATCCC ACYTCTTTGC ATGGGAMCCT GTGCCAAACA CCCAAGTTTA        960

AGARAARARY ARARCTGWGG CAGGTATACA GAGCTGGAAG TGGACCATGG AAAACATSGA       1020

TAACCATGCA TCYTCTTGCT TGGCCACCTC CTGAAACTGT CCACCTTTGA AGTTTGAACT       1080

TTAGTCCCTC CAMACTCTGA CTGCTGCCTC CTTCCTCCCA GCTCTCTCAC TGAGTTATYT       1140

TCACTGTACC TGTTCCAGCA TATCCCCACT ATCTCTCTTT CTCCTGATCT GTGCTGTCTT       1200

ATTCTCCTCC TTAGGCTTCC TATTACCTGG GATTCCATGA TTCATTCCTT CAGACCCTCT       1260

CCTGCCAGTA TGCTAAACCC TCCCTCTCTC TTTCTTATCC CGCTGTCCCA TTGGCCCAGC       1320

CTGGATGAAT CTATCAATAA AACAACTAGA GAATGGTGGT CAAAAAAAAA AAAAAAAAAC       1380

TCGA                                                                   1384
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(2) INFORMATION FOR SEQ ID NO: 225:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 760 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

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GGGTCGACCC ACGCGTCCGC TGACCAGTCC GTTATAGATA CTTCTTCCTA TACCAAAACT         60

GTTTAAACAG GTGCCACCAC AAGGGATGTC GTCCTTACTC TCTGCGGGTC TTCAAGCATC        120

CCTTTGTGGG AAARGTCTCT GGGCAAGCAC GTGGTATTTG GTCTGCTGCT TGCTTCCCTT        180

TTTCCACCAG GGATGTTGTG ATCATAAGTC AAAACAACAG TATATTCCAA ATCTCAAAAG        240

CTATTGTGGC CTGAGCACAA TTGAAATCTA GCAGAGTTTT TCCTATGTAG CTTTAGAGTA        300

ACTCTTCTGC TTCTCTGTCA CTTACAATTC AGGTTCTGCC TTTGCCTAAG AGCATGAGCA        360

GAAGAGTCCT CATGTGACGC TTAGTTCTAT TGCAGTCCTG GGTGAAACTA TTTAAGCWAT        420

GGGGCTGCTK CTCCCCANWT CCTCCCTAAC AATTCGTTGT GTGGACTTCT CATCTAAAAG        480

GTTAGTGGCT TTTGCTTGGG ATCAGTGCTC TCTATTGATG TTCTTGCTGG TCTCCAGACA        540

CATTCCTGTT GCATTAAGAC TTGAAAGACT TGTAGATGTG TGATGTTCAG GCACAGGATG        600

CTGAAAGCTA TGTTACTATT CTTAGTTTGT AAATTGTCCT TTTGATACCA TCATCTTGTT        660

TTCTTTTTGT AGGTATAAAT AAAAACACTG TTGACAATAA AAAAAAAAAA AAAAAAAAAA        720

AAAAAAAAAA AAAAAAAAAA NAAAAAAAAA AAAAAAAAAA                              760
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(2) INFORMATION FOR SEQ ID NO: 226:

5   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 2057 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: double
                    (D) TOPOLOGY: linear
10
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

    CCGAGCCGGC TGCGCCGGGG GAATCCGTGC GGGCGCCTTC CGTCCCRGTC CCATCCTCGC   60

15 CGCGCTCCAG CACCTCTGAA GTTTTGCAGC GCCCAGAAAG GAGGCGAGGA AGGAGGGAGT   120

    GTGTGAGAGG AGGGAGCAAA AAGCTCACCC TAAAACATTT ATTTCAAGGA GAAAAGAAAA   180

20 AGGGGGGGCG CAAAAATGGC TGGGGCAATT ATAGAAAACA TGAGCACCAA GAAGCTGTGC   240

    ATTGTTGGTG GGATTCTGCT CGTGTTCCAA ATCATCGCCT TTCTGGTGGG AGGCTTGATT   300

    GCTCCAGGGC CCACAACGGC AGTGTCCTAC ATGTCGGTGA AATGTGTGGA TGCCCGTAAG   360

25 AACCATCACA AGACAAAATG GTTCGTGCCT TGGGGACCCA ATCATTGTGA CAAGATCCGA   420

    GACATTGAAG AGGCAATTCC AAGGGAAATT GAAGCCAATG ACATCGTGTT TTCTGTTCAC   480

30 ATTCCCCTCC CCACATGGA GATGAGTCCT TGGTTCCAAT TCATGMTGTT TATCCTGCAG   540

    CTGGACATTG CCTTCAAGCT AAACAACCAA ATCAGRGAAA ATGCAGAAGT CTCCATGGAC   600

    GTTTCCCTGG CTTACCGTGA TGACGCGTTT GCTGAGTGGA CTGAAATGGC CCATGAAAGA   660

35 GTACCACGGA AACTCAAATG CACCTTCACA TCTCCCAAGA CTCCAGAGCA TGGAGGGCCG   720

    GTTACTATGA ATGTGATGTC CTTCCTTTCA TGGAAATTGG GTCTGTGGCC CATGAAGTTT   780

    TACCTTTTAA ACATCCGGCT GCCTGTGAAT GAGAAGAAGA AAATCAATGT GGGAATTGGG   840

40 GAGATAAAGG ATATCCGGTT GGTGGGGATC CACCAAAATG GAGGCTTCAC CAAGGTGTGG   900

    TTTGCCATGA AGACCTTCCT TACGCCCAGC ATCTTCATCA TTATGGTGTG GTATTGGAGG   960

45 AGGATCACCA TGATGTCCCG ACCCCCAGTG CTTCTGGAAA AAGTCATCTT TGCCCTTGGG   1020

    ATTTCCATGA CCTTTATCAA TATCCCAGTG GAATGGTTTT CCATCGGGTT TGACTGGACC   1080

50 TGGATGCTGC TGTTTGGTGA CATCCGACAG GCATCTTCTA TGCRATGCTT CTKTCCTTCT   1140

    GGATCATCTT CTGTGGCGAG CACATGATGG ATCAGCACGA GCGGAACCAC ATCGCAGGGT   1200

    ATTGGAAGCA AGTCGGACCC ATTGCCGTTG GTCCTTCTGC CTCTTCATAT TTGACATGTG   1260

55 TGAGAGAGGG GTACAACTCA CGAATCCCTT CTACAGTATC TGGACTACAG ACATTGGGAA   1320

    CAGAGCTGGC CATGGCTTTC ATCATCGTGG CTGGAATCTG CCTCTGCCTC TAACTTCCTG   1380

    TTTCTATGCT TCATGGTATT TCAGGTGTTT CGGAACATCA GTGGAAGCA GTCCAGCCTG   1440

60

479

CCAGCTATGA GCAAGTCCG GCGGCTACAC TATGAGGGGC TAATTTTTAG GTTCAAGTTC   1500

CTCATGCTTA TCACCTTGGC TTGCGCTGCC ATGACTGTCA TCTTCTTCAT CGTTAGTCAG   1560

GTAACGGAAG GCTATTGGGA AATGGGGCGG CGTCACAGTC CCAAGTGAAC AGTGCCTTTT   1620

TCACAGGCAT CTATGGGATG TGGAATCTGT ATGTCTTTGC TCTGATGTTC TTGTATGCAC   1680

CATCCCATAA AAACTATGGA GAAGACCAGT CCAATGGAAT GCAACTCCCA TGTAAATCGA   1740

GGGAAGATTG TGCTTTGTTT GTTTCGGAAC TTTATCAAGA ATTGTTCAGC GCTTCGAAAT   1800

ATTCCTTCAT CAATGACAAC GTAGCTTCTG GTATTTGAGT CAACAAGGCA ACACATGTTT   1860

ATCAGCTTTG CATTTGCAGT TGTCACAGTC ACATTGATTG TACTTGTATA CGCACACAAA   1920

TACACTCATT TAGCCTTTAT CTCAAAATGT TAAATATAAG GAAAAAAGCG TCAACAATAA   1980

ATATTCTTTG AGTATTGTCT TACTTCTCTT AAAAAAAAA AAAAAAACTC GTGCCGAATT   2040

CGGCACGAGC GGCACGA   2057

(2) INFORMATION FOR SEQ ID NO: 227:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 2084 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GGCAGAGGGC CATTTCCTGC AAAGAGCCAA ACCCCCATTC CTCTGTGCCC CTCCTCTCCC   60

ACCAAGTGCT TTATAAAAT ACCTCTTGTT ACCGGAAATA ACTGTTCATT TTTCACTCCT   120

CCCTCCTAGG TCACACTTTT CAGAAAAGA ATCTGCATCC TGGAAACCAG AAGAAAAATA   180

TGAGACGGGG AATCATCGTG TGATGTGTGT SCTGCCTTTG GCTGAGTGTG TGGAGTCCTG   240

CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG AGGGGAACCG CTTGTTCAGA   300

GCTGTGACTG CGGCTGCACT GCAGAGAAGC TGCCCTTGGC TGCTCGTAGC GCCGGGCCTT   360

CTCTCCTCGT CATCATCCAG AGCAGCCAGT GTCCGGGAGG CAGAAGGTAC CGGGGCAGCT   420

ACTGGAGGAC TGTGCGGCCC TGCCTGGGCT GCCCCCTCCG CCGTGGGGCC CTGTTGCTGC   480

TGTCCATCTA TTTCTACTAC TCCCTCCCAA ATGCGGTCGG CCCGCCCTTC ACTTGGATGC   540

TTGCCCTCCT GGGCCTTCTC GCAGGCACTG AACATCCTCC TGGGCCTCAA GGGCCTGGCC   600

CCAGCTGAGA TCTCTGCAGT GTGTGAAAAA GGGAATTTCA ACGTGGCCCA TGGGCTGGCA   660

TGGTCATATT ACATCGGATA TCTGCGGCTG ATCCTGCCAG AGCTCCAGGC CCGGATTCGA   720

ACTTACAATC AGCATTACAA CAACCTGCTA CGGGGTGCAG TGAGCCAGCG GTGTNATATT   780

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CTCCTCCCAT TGGACTGTGG GGTGCCTGAT AACCTGAGTA TGGCTGACCC CAACATTCGC          840

TTCCTGGATA AACTGCCCCA GCAGACCGGT GACCGTGCTG GCATCAAGGA TCGGGTTTAC          900

AGCAACAGCA TCTATGAGCT TCTGGAGAAC GGGCAGCGGG CGGGCACCTG TGTCCTGGAG          960

TACGCCACCC CCTTGCAGAC TTTGTTTGCC ATGTCACAAT ACAGTCAAGC TGGCTTTAGC         1020

GGGGAGGATA GGCTTGAGCA GGCCAAACTC TTCTGCCGGA CACTTGAGGA CATCCTGGCA         1080

GATGCCCCTG AGTCTCAGAA CAACTGCCGC CTCATTGCCT ACCAGGAACC TGCAGATGAC         1140

AGCAGCTTCT CGCTGTCCCA GGAGGTTCTC CGGCACCTGC GGCAGGAGGA AAAGGAAGAG         1200

GTTACTGTGG GCAGCTTGAA GACCTCAGCG GTGCCCAGTA CCTCCACGAT GTCCCAAGAG         1260

CCTGAGCTCC TCATCAGTGG AATGGAAAAG CCCCTCCCTC TCCGCACGGA TTTCTCTTGA         1320

GACCCAGGGT CACCAGGCCA GAGCCTCCAG TGGTCTCCAA GCCTCTGGAC TGGGGGCTCT         1380

CTTCAGTGGC TGAATGTCCA GCAGAGCTAT TTCCTTCCAC AGGGGGCCTT GCAGGGAAGG         1440

GTCCAGGACT TGACATCTTA AGATGCGTCT TGTCCCCTTG GGCCAGTCAT TTCCCCTCTC         1500

TGAGCCTCGG TGTCTTCAAC CTGTGAAATG GGATCATAAT CACTGCCTTA CCTCCCTCAC         1560

GGTTGTTGTG AGGACTGAGT GTGTGGAAGT TTTTCATAAA CTTTGGATGC TAGTGTACTT         1620

AGGGGGTGTG CCAGGTGTCT TTCATGGGGC CTTCCAGACC CACTCCCCAC CCTTCTCCCC         1680

TTCCTTTGCC CGGGGACGCC GAACTCTCTC AATGGTATCA ACAGGCTCCT TCGCCCTCTG         1740

GCTCCTGGTC ATGTTCCATT ATTGGGGAGC CCCAGCAGAA GAATGGAGAG GAGGAGGAGG         1800

CTGAGTTTGG GGTATTGAAT CCCCCGGCTC CCACCCTGCA GCATCAAGGT TGCTATGGAC         1860

TCTCCTGCCG GGCAACTCTT GCGTAATCAT GACTATCTCT AGGATTCTGG CACCACTTCC         1920

TTCCCTGGCC CCTTAAGCCT AGCTGTGTAT CGGCACCCCC ACCCCACTAG AGTACTCCCT         1980

CTCACTTGCG GTTTCCTTAT ACTCCACCCC TTTCTCAACG GTCCTTTTTT AAAGCACATC         2040

TCAGATTAAA AAAAAAAAA AAAAAAAAA AGGGGGGGCN GCNT                           2084
```

(2) INFORMATION FOR SEQ ID NO: 228:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2143 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
TCGACCCACG CGTCCGGTTG AATTCCTTGA CCTGCAAACA CATATTTATT AGCCTGACTC           60
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AAACAATGAA GCTATTAAAA CTTCGGAGGA ACATTGTAAA ACTCTCTTTG TATCGGCATT   120

TCACCAACAC GCTTATTTTG GCAGTGGCAG CATCCATTGT GTTTATCATC TGGACAACCA   180

TGAAGTTCAG AATAGTGACA TGTCAGTCGG ACTGGCGGGA GCTGTGGGTA GACGATGCCA   240

TCTGGCGCTT GCTGTTCTCC ATGATCCTCT TTGTCATCAT GGTTCTCTGG CGACCATCTG   300

CAAACAACCA GAGGTTTGCC TTTTCACCAT TGTCTGAGGA AGAGGAGGAG GATGAACAAA   360

AGGAGCCTAT GCTGAAAGAA AGCTTTGAAG GAATGAAAAT GAGAAGTACC AAACAAGAAC   420

CCAATGGAAA TAGTAAAGTT AACAAAGCAC AGGAAGATGA TTTGAAGTGG GTAGAAGAGA   480

ATGTTCCTTC TTCTGTGACA GATGTAGCAC TTCCAGCCCT TCTGGATTCA GATGAGGAAC   540

GAATGATCAC ACACTTTGAA AGGTCCAAAA TGGAGTAAGG AATGGGAAGA TTTGCAGTTA   600

AAGATGGCTA CCATCAGGGA AGAGATCAGC ATCTGTGTCA GTCTTCTGTA CGGCTCCATG   660

GGATTAAAGG AAGCAATGAC ATCCTGATCT GTTCCTTGAT CTTTGGGCAT TGGAGTTGGC   720

GAGAGGTGTC AGAACAAAGA GAACATCTTA CTGAAAACAA GTTCATAAGA TGAGAAAAAT   780

CTACGAGCTT CTTATTTACA ACACTGCTGC CCCCTTTCCT CCCAGACTCT GACATGGATG   840

TTCATGCAAC TTAAGTGTGT TGTTCCTGAA CTTTCTGTAA TGTTTCATTT TTTAAATCTG   900

ACAAACTAAA AAGTTTAACG TCTTCTAAAA GATTGTCATC AACACCATAA TATGTAATCT   960

CCAGGAGCAA CTGCCTGTAA TTTTTATTTA TTTAGGGAGT TACATAGGTG ATGGGGGAAA   1020

TTGTTAACTA CCTTTCATTT TCCTGGGAAG TCAAGGTTAC ATCTTGCAGA GGTTGTTTTG   1080

AGAAAAAAGG GCCCTTCTGA GTTAAGGAGC CATAGTTCTA TCAATGATCA AAAGAAAAAA   1140

AAAAAAAAGA GAAACTGTTA CAGTATGATT CAGATCATTT AAAAAAGCAA AATCAAGTGC   1200

AATTTTGTTT ACAAATGGTG TATATTAAAG ATTTTTCTAT TTCAGATGTA CTTTAAAGAG   1260

AAATATTAGC TTAACTCTTT TGACATCTGC TATTGTGACA CATCCCATTG CTGGCAATGT   1320

GGTGCACACT CCGAAACTTT TAACTACTGT TTTGTAAGCC TCCAAGGGTG GCATTGCAGG   1380

GTCCTTAGGC AATGTTTTGT TTGCCTTTAT GCAGAGAGGT GCTCCAAGTG CTGTGATTGA   1440

GCACCGTGCT AGAGGAACTG TAATGCTTCA GAAGTTGTAG CTTATACAAA GGAAACAGGT   1500

CCTGCTGGCT TAATTTAAAC AGTTATTGCA TGAAGTAGCG TGGAGGCCCT GGACTGCTGC   1560

TCGTTCTTTA GGATGGACTG TTCTGGTATC TGGTATTGGT TTAGAGACTG TTAATAAGGG   1620

ACATCACAAG GTGATGGGAT TCATTTGAAG CACTCTATTT CTGTTTTAAT GGTTTTATCC   1680

AATTTTGCCT TCCCAAGATT TTTGTTCTAC ATAAAAAGTT CATGCCACTT TTTAATATAA   1740

AAAAATTTAA CAAAATTAAT GTATTTTTCT CATTTTTTTC AAACTTTTTC TAAAGACTCT   1800

TTCTGTCAAA CTCATGAAAA ATTTCTTTCT ATGGCTTTTA TTCTAGATTG TCTTATTTTC   1860

TGTTAAAACC AATGACCACA TGACCACAAT CTTCACTAAC TCATACTGCA GTGAAAGTGT   1920

TAACCCTTAG GTAGTTTCTC TACAACTCTT TGCTATGGTG ATTTTTAAAA AAGTTTCCTA   1980

GGGAAGTATC TCTGAGGGAA CAGGCAATCT GAAGGAACTG ACTATATTCT CCATGGCTAA   2040

GTCCATTAGG CCAAAAGNCT GGGTGGGTAT TGGTTGTCAN GCTGTCTATT GGCATATTAA   2100

AAACGTAGGC CGGANGGAAT AATTAGGTTG TNATGCCGGC GGG   2143

(2) INFORMATION FOR SEQ ID NO: 229:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1025 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCTGGCCCAC ATTGCTTCAT TGGCCTGGCC ATGCGCCTGT ACTATGGCAG CCGCTAGTCC   60

CTGACAACTT CCACCCTGAT TCCGGACCCT GTAGATTGGG CGCCACCACC AGATCCCCCT   120

CCCAGGCCTT CCTCCCTCTC CCATCAGCAG CCCTGTAACA AGTGCCTTGT GAGAAAAGCT   180

GGAGAAGTGA GGGCAGCCAG GTTATTCTCT GGAGGTTGGT GGATGAAGGG GTACCCTAGG   240

AGATGTGAAG TGTGGGTTTG GTTAAGGAAA TGCTTACCAT CCCCCACCCC CAACCAAGTT   300

CTTCCAGACT AAAGAATTAA GGTAACATCA ATACCTAGGC CTGAGAAATA ACCCCATCCT   360

TGTTGGGCAG CTCCCTGCTT TGTCCTGCAT GAACAGAGTT GATGAAAGTG GGGTGTGGGC   420

AACAAGTGGC TTTCCTTGCC TACTTTAGTC ACCCAGCAGA GCCACTGGAG CTGGCTAGTC   480

CAGCCCAGCC ATGGTGCATG ACTCTTCCAT AAGGGATCCT CACCCTTCCA CTTTCATGCA   540

AGAAGGCCCA GTTGCCACAG ATTATACAAC CATTACCCAA ACCACTCTGA CAGTCTCCTC   600

CAGTTCCAGC AATGCCTAGA GACATGCTCC CTGCCCTCTC CACAGTGCTG CTCCCCACAC   660

CTAGCCTTTG TTCTGGAAAC CCCAGAGAGG GCTGGGCTTG ACTCATCTCA GGGAATGTAG   720

CCCCTGGGCC CTGGCTTAAG CCGACACTCC TGACCTCTCT GTTCACCCTG AGGGCTGTCT   780

TGAAGCCCGC TACCCACTCT GAGGCTCCTA GGAGGTACCA TGCTTCCCAC TCTGGGGCCT   840

GCCCCTGCCT AGCAGTCTCC CAGCTCCCAA CAGCCTGGGG AAGCTCTGCA CAGAGTGACC   900

TGAGACCAGG TACAGGAAAC CTGTAGCTCA ATCAGTGTCT CTTTAACTGC ATAAGCAATA   960

AGATCTTAAT AAAGTCTTCT AGGCTGTAGG GTGGTTCCTA CAACCACAGC CAAAAAAAAA   1020

AAAAA   1025

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(2) INFORMATION FOR SEQ ID NO: 230:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1250 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
GCCCACGCGT CCGCCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG        60

GGCTACTGGC GCTTCCTGGC GCYGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCGGTG       120

ATSTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA       180

CTAGAGTTTA ACTGGCACCC AGTGCTSATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC       240

GCATCATCGT CTACAGACTG CCGTGGACCT GGAAATGCAG CAAGCTCCTG ATGAAATCCA       300

TCCATGCAGG GTTAAATGCA GTTGCTGCCA TTCTTGCAAT TATCTCTGTG GTGGCCGTGT       360

TTGAGAACCA CAATGTTAAC AATATAGCCA ATATGTACAG TCTGCACAGC TGGGTTGGAC       420

TGATAGCTGT CATATGCTAT TTGTTACAGC TTCTTTCAGG TTTTTCAGTC TTTCTGCTTC       480

CATGGGCTCC GCTTTCTCTC CGAGCATTTC TCATGCCCAT ACATGTTTAT TCTGGAATTG       540

TCATCTTTGG AACAGTGATT GCAACAGCAC TTATGGGATT GACAGAGAAA CTGATTTTTT       600

CCCTGAGAGA TCCTGCATAC AGTACATTCC CGCCAGAAGG TGTTTTCGTA AATACGCTTG       660

GCCTTCTGAT CCTGGTGTTC GGGGCCCTCA TTTTTTGGAT AGTCACCAGA CCGCAATGGA       720

AACGTCCTAA GGAGCCAAAT TCTACCATTC TTCATCCAAA TGGAGGCACT GAACAGGGAG       780

CAAGAGGTTC CATGCCAGCC TACTCTGGCA ACAACATGGA CAAATCAGAT TCAGAGTTAA       840

ACARTGAAGT AGCAGCAAGG AAAAGAAACT TAGCTCTGGA TGAGGCTGGG CAGAGATCTA       900

CCATGTAAAA TGTTGTAGAG ATAGAGCCAT ATAACGTCAC GTTTCAAAAC TAGCTCTACA       960

GTTTTGCTTC TCCTATTAGC CATATGATAA TTGGGCTATG TAGTATCAAT ATTTACTTTA      1020

ATCACAAAGG ATGGTTTCTT GAAATAATTT GTATTGATTG AGGCCTATGA ACTGACCTGA      1080

ATTGGAAAGG ATGTGATTAA TATAAATAAT AGCAGATATA AATTGTGGTT ATGTTACCTT      1140

TATCTTGTTG AGGACCACAA CATTAGCACG GTGCCTTGTG CAKAATAGAT ACTCAATATG      1200

TGAATATGTG TCTACTAGTA GTTAATTGGA TAAACTGGCA GCATCCCTGA                1250
```

(2) INFORMATION FOR SEQ ID NO: 231:

       (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1811 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```
CNGNCAGTAC CGGTCNGATT CCCGGGTCGA CCCACGCGTC CGCTGCATTC CAGGGCCTTT      60

CAGTGGCTTT CATTCTGAAG TTCCTGGATA ACATGTTCCA TGTCTTGATG GCCCAGGTTA     120

CCASTGTCAT TATCACAACA GTGTCTGTCC TGGTCTTTGA CTTCAGGCCC TCCCTGGAAT     180

TTTTCTTGGA AGCCSCATCA GTCSTYCTCT CTATATTTAT TTATAATGCC AGCAAGCCTC     240

AAGTTCCGGA ATACGCACCT AGGCAAGAAA GGATCCGAGA TCTAAGTGGC AATCTTTGGG     300

AGCGTTCCAG TGGGGATGGA GAAGAACTAG AAAGACTTAC CAAACCCAAG AGTGATGAGT     360

CAGATGAAGA TACTTTCTAA CTGGTACCCA CATAGTTTGC AGCTCTCTTG AACCTTATTT     420

TCACATTTTC AGTGTTTGTA ATATTTATCT TTTCACTTTG ATAAACCAGA AATGTTTCTA     480

AATCCTAATA TTCTTTGCAT ATATCTAGCT ACTCCCTAAA TGGTTCCATC CAAGGCTTAG     540

AGTACCCAAA GGCTAAGAAA TTCTAAAGAA CTGATACAGG AGTAACAATA TGAAGAATTC     600

ATTAATATCT CAGTACTTGA TAAATCAGAA AGTTATATGT GCAGATTATT TTCCTTGGCC     660

TTCAAGCTTC CAAAAAACTT GTAATAATCA TGTTAGCTAT AGCTTGTATA TACACATAGA     720

GATCAATTTG CCAAATATTC ACAATCATGT AGTTCTAGTT TACATGCCAA AGTCTTCCCT     780

TTTTAACATT ATAAAAGCTA GGTTGTCTCT TGAATTTTGA GGCCCTAGAG ATAGTCATTT     840

TGCAAGTAAA GAGCAACGGG ACCCTTTCTA AAAACGTTGG TTGAAGGACC TAAATACCTG     900

GCCATACCAT AGATTTGGGA TGATGTAGTC TGTGCTAAAT ATTTTGCTGA AGAAGCAGTT     960

TCTCAGACAC AACATCTCAG AATTTTAATT TTTAGAAATT CATGGGAAAT TGGATTTTTG    1020

TAATAATCTT TTGATGTTTT AAACATTGGT TCCCTAGTCA CCATAGTTAC CACTTGTATT    1080

TTAAGTCATT TAAACAAGCC ACGGTGGGGC TTTTTTCTCC TCAGTTTGAG GAGAAAAATC    1140

TTGATGTCAT TACTCCTGAA TTATTACATT TTGGAGAATA AGAGGGCATT TTATTTTATT    1200

AGTTACTAAT TCAAGCTGTG ACTATTGTAT ATCTTTCCAA GAGTTGAAAT GCTGGCTTCA    1260

GAATCATACC AGATTGTCAG TGAAGCTGAT GCCTAGGAAC TTTTAAAGGG ATCCTTTCAA    1320

AAGGATCACT TAGCAAACAC ATGTTGACTT TTAACTGATG TATGAATATT AATACTCTAA    1380

AAATAGAAAG ACCAGTAATA TATAAGTCAC TTTACAGTGC TACTTCACAC TTAAAAGTGC    1440

ATGGTATTTT TCATGGTATT TTGCATGCAG CCAGTTAACT CTCGTAGATA GAGAAGTCAG    1500

GTGATAGATG ATATTAAAAA TTAGCAAACA AAAGTGACTT GCTCAGGGTC ATGCAGCTGG    1560

GTGATGATAG AAGAGTGGGC TTTAACTGGC AGGCCTGTAT GTTTACAGAC TACCATACTG    1620
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TAAATATGAG CTTTATGGTG TCATTCTCAG AAACTTATAC ATTTCTGCTC TCCTTTCTCC          1680

TAAGTTTCAT GCAGATGAAT ATAAGGTAAT ATACTATTAT ATAATTCATT TGTGATATCC          1740

ACAATAATAT GACTGGCAAG AATTGGTGGA AATTTGTAAT TAAAATAATT ATTAAACCTA          1800

AAAAAAAAAN N                                                               1811
```

(2) INFORMATION FOR SEQ ID NO: 232:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 2271 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
CTGACCTCAT GGCGTAGAGC CTAGCAACAG CGCAGGCTCC CAGCCGAGTC CGTTATGGCC          60

GCTGCCGTCC CGAAGAGGAT GAGGGGGCCA GCACAAGCGA AACTGCTGCC CGGGTCGGCC          120

ATCCAAGCCC TTGTGGGGTT GGCGCGGCCG CTGGTCTTGG CGCTCCTGCT TGTGTCCGCC          180

GCTCTATCCA GTGTTGTATC ACGGACTGAT TCACCGAGCC CAACCGTACT CAACTCACAT          240

ATTTCTACCC CAAATGTGAA TGCTTTAACA CATGAAAACC AAACCAAACC TTCTATTTCC          300

CAAATCAGCA CCACCCTCCC TCCCACGACG AGTACCAAGA AAAGTGGAGG AGCATCTGTG          360

GTCCCTCATC CCTCGCCTAC TCCTCTGTCT CAAGAGGAAG CTGATAACAA TGAAGATCCT          420

AGTATAGAGG AGGAGGATCT TCTGATGCTG AACAGTTCTC CATCCACAGC CAAAGACACT          480

CTAGACAATG GCGATTATGG AGAACCAGAC TATGACTGGA CCACGGGCCC CAGGGACGAC          540

GACGAGTCTG ATNGACACCT TGGAAGAAAA CAGGGGTTAC ATGGAAATTG AACAGTCAGT          600

GAAATCTTTT AAGATGCCAT CCTCAAATAT AGAAGAGGAA GACAGCCATT TCTTTTTTCA          660

TCTTATTATT TTTGCTTTTT GCATTGCTGT TGTTTACATT ACATATCACA ACAAAAGGAA          720

GATTTTTCTT CTGGTTCAAA GCAGGAAATG GCGTGATGGC CTTTGTTCCA AAACAGTGGA          780

ATACCATCGC CTAGATCAGA ATGTTAATGA GGCAATGCCT TCTTTGAAGA TTACCAATGA          840

TTATATTTTT TAAAGCACTG TGATTTGAAT TTGCTTATGT AATTTTATTT GCTTGACTTT          900

TTATATGATA TTGTGCAAAT GTTTGCCATA GGCAATTGGT ACTTAAATGA GAGGTGAGTC          960

TCTCTTTTGC CTTGGTGCTT TGGAAATTAA ATGTCACAAA CGAGTATATA ATTTTTTATC          1020

TGTACTTTTA GAGCTGAGTT TAATCAGGTG TCCAAAATGT GAGTTAAACA TTACCTTATA          1080

TTTACACTGT TAGTTTTTAT TGTTTTAGAT TTATTATGCT TCTTCTGGAA GTATTAGTGA          1140
```

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TGCTACTTTT AAAAGATCCC AAACTTGTAA CTAAATTCTG ACATATCTGT TACTGCTGAC      1200

TCACATTCAT TCTCCGCCAT TCAAATACTA TTTTTTATCC ACATTTTTTT TTGTTCCCAA      1260

ACTGTAATGT ACAAGGATAT GTGTGATAAT GCTTTGGATT TGAGTAATAT TTTTTTTTCT      1320

TCCAAGAAAA CTGCTTTGGA TATTTTTAGA TAATTTAAAC ATAATTTAGG ATAATGATAT      1380

TGCTCAATCT GACCACAATT TTAGGTAAAA CATTAAATGT GTCAAGAAAT CTTGGCAACA      1440

GAGACTCTGC AGCTTGCAGT GGACATAGAT AAAATGTTAC AGAGATACTA TTTTTTTGGT      1500

TGGAATTACT ATATTAAATT TAGAAGCAGA AACTGGTAAA ATGTTAAATA CATGTACAAT      1560

TGCTTTTAGT TAGCAATTGA TTGTAGCATG GGTTCCTCCA AGGTTTCAAG CAATGGGCAG      1620

AGTTTAAAAT TATATCAGAT TCGTTTACTT CGTTTATTAT TTTACAGTAA ATTTGAATAA      1680

ATCTTAGGGG TCATTATCAC TTAAATAATA CTGTACCTAG GTCTTTCAAA TTAAAATTAT      1740

ACCTGAATGA AGTTGTTTGT ATACATAAAG GATATTTGTG TACAATTACC TTTTTTCCCC      1800

CACACTTGTT TTCTTTGTTT TTGTTTTTTA TGGCAACTGG AAAGTATTTA CTATGGGATT      1860

CATTTATGTC TGTCTTTCTA TCATAAAGAA TTGATCAATA TGTAAATATG TGATTTGAAC      1920

CATGGTTGAC TTACAAGTGT CACTACAGCT TTTTAGAAAA CATAGCCCTA ATATATGTTA      1980

AGCAGGACCC GGGTGAGCCA GTGGGCTTGC GCTTTATGTA GAGCTGGAAG AAGGCCGTCC      2040

ATCCTGTCTC TTGGGCGGAC AGTGTACTTT CCTAATAGGG AAGGGAAGCA CAATGGAAAT      2100

ACCCCTGAAC CGTTTTATTG CAGTAATTTT TTTCATATCT GAAACTATTA TTTAATATTT      2160

TGAATAAGAT TTTAAAAAAT AAATGGCAAA GATATAAATC TAAAAAAAAA AAAAAAAAA       2220

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAANANA N              2271
```

(2) INFORMATION FOR SEQ ID NO: 233:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1338 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC       60

TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA      120

GCCAGCGTGG CGNGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG      180

GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTTG      240

CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT      300
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YTTGGGCCTC CTGACCCCTAG ACCAGGACAT TACCGCCGCT GCCACCGGGC CCTWACCCCT   360

GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGG CCGCGGGGCT CCGAGGGAGG   420

CAATGGCAGC AACCCTGTGG CCGGGCTTGA GACGGACGAT CACGGAGGGA AGGCCGGGGA   480

ARGCTCGGTG GGTGGCGGCC TTGCTGTGAG CCCCAACCCT GGCGACAAGC CCATGACCCA   540

GCGGGCCCTG ACCGTGTTGA TGGTGGTGAG CGGCGCGGTG CTGGTGTACT TCGTGGTCAG   600

GACGGTCAGG ATGAGAAGAA GAAACCGAAA GACTAGGAGA TATGGAGTTT TGGACACTAA   660

CATAGAAAAT ATGGAATTGA CACCTTTAGA ACAGGATGAT GAGGATGATG ACAACACGTT   720

GTTTGATGCC AATCATCCTC GAAGATAAGA ATGTGCCTTT TGATGAAAGA ACTTTATCTT   780

TCTACAATGA AGAGTGGAAT TTCTATGTTT AAGGAATAAG AAGCCACTAT ATCAATGTTG   840

GGGGGGTATT TAAGTTACAT ATATTTNAAC AACCTTTAAT TTGCTGTTGC AATAAATACC   900

GTATCCTTTT ATTATATCTT TATATGTATA GAAGTACTCT GTTAATGGGC TCAGAGATGT   960

TGGGGATAAA GTATACTGTA ATAATTTATC TGTTTGAAAA TTACTATAAA ACGGTGTTTT   1020

CTGRTCGGTT TTTGTTTCCT GCTTACCATA TGATTGTAAA TTGTTTTATG TATTAATCAG   1080

TTAATGCTAA TTATTTTTGC TGATGTCATA TGTTAAAGAG CTATAAATTC CAACAACCAA   1140

CTGGTGTGTA AAAATAATTT AAAATYTCCT TTACTGAAAG GTATTTCCCA TTTTTGTGGG   1200

GAAAAGAAGC CAAATTTATT ACTTTGTGTT GGGGTTTTTA AAATATTAAG AAATGTCTAA   1260

GTTATTGTTT GCAAAACAAT AAATATGATT TTAAATTCTC TTAAAAAAAA AAAAAAAAC   1320

CCCGGGGGGG GGCCCGGN   1338

(2) INFORMATION FOR SEQ ID NO: 234:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 31 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Met Leu Ser Thr Gly Ile Glu Val Ala Arg Pro Pro Ala Thr Leu Leu
 1   5   10   15

Gly Leu Met Phe Val Leu Thr Gly Met Pro Arg Gly Leu Arg Xaa
            20   25   30

(2) INFORMATION FOR SEQ ID NO: 235:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 116 amino acids

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```
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Asn Val Val Ile Val Ile Ile Leu Phe Ser Phe Asp Ser Val Gly
 1               5                 10                15

Thr Met Phe Ser Cys Asn Arg Ile Pro Lys Ile Thr Val Leu Asn Lys
             20             25             30

Leu Lys Phe Xaa Cys Glu Val Leu Leu Arg Ile Gln Thr Ile Gln Gly
         35             40             45

Phe Tyr Arg Cys Thr Arg Ile Ser Arg Tyr Lys Gly Ile Phe Pro Asp
     50             55             60

Phe Cys Gln Ser Gln Cys Met Gly Cys Asn Pro Glu Ser Xaa Met Ala
 65             70             75             80

Val Pro Ala Leu Val Thr Pro Ile Leu Ala His Arg Lys Lys Glu Lys
             85             90             95

Gly Met Cys Leu Phe Thr Leu Ile Ile Ala Pro Thr Arg Cys Thr His
         100            105            110

Tyr Phe Cys Xaa
         115
```

(2) INFORMATION FOR SEQ ID NO: 236:

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 103 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Ser Ser Ala Lys Ile Val Arg Gln Arg Gly Ala Val Pro Thr Tyr
 1               5                 10                15

Tyr Thr Thr Glu Ala Gly Glu Ile Ile Phe Leu Val Leu Asn Trp Ser
             20             25             30

Leu Ser Ile Leu His Ile Val Asp Val Leu Cys Ser Lys Pro Glu Lys
         35             40             45

Ser Val Thr Glu Asp Ala Ala Ser Gly Leu Ser Gln Arg Met Thr Ala
     50             55             60

Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys Pro Ile Leu
 65             70             75             80

Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His Ser Phe Ile
             85             90             95

His Ser Ser Asn Ile Cys Xaa
         100
```

489

(2) INFORMATION FOR SEQ ID NO: 237:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 42 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Ile Leu Phe Pro Gln Xaa Ala Leu Arg Leu Gly Xaa Trp Pro Arg
1   5   10   15

Thr Trp Ser Ile Leu Xaa Lys Tyr Ser Val Asn Phe Phe Ser Ala Tyr
            20   25   30

Ser Pro Met Gly Ala Val Gly Thr Glu Phe
        35   40

(2) INFORMATION FOR SEQ ID NO: 238:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 37 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Met Ile Ile Leu Leu Leu Phe Met Leu Leu Asn Asn Val Val Leu Val
1   5   10   15

Gln Glu Asp Asn Cys Gln Arg Lys Asn Thr Val Gln Glu Arg Arg Xaa
            20   25   30

Trp Ser Gln Trp Xaa
        35

(2) INFORMATION FOR SEQ ID NO: 239:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 128 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Met Ala Ala Xaa Pro Pro Gly Cys Thr Pro Pro Xaa Leu Leu Asp Ile
1   5   10   15

Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu
            20   25   30

Cys Arg His Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser
        35   40   45

Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr
        50   55   60

His His Asn Thr Gly Leu Ser Glu Leu Leu Glu His Gly Val Cys Glu

490

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        65                  70                  75                  80

        Glu Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Val
                        85                  90                  95
5

        Arg Arg Ala Gly Leu Gly Pro Thr Pro Gly Met Ser Cys Pro Gly Asn
                100                 105                 110

        Asp Asn Thr Val His Thr Met His Gly Glu Ala Asn Arg Gly Ser Xaa
10              115                 120                 125




15


        (2) INFORMATION FOR SEQ ID NO: 240:

                (i) SEQUENCE CHARACTERISTICS:
20                      (A) LENGTH: 67 amino acids
                        (B) TYPE: amino acid
                        (D) TOPOLOGY: linear
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

25      Met Ser Ile Leu Cys Cys Pro Xaa Leu Cys Leu Phe Phe Ser Phe Cys
          1               5                  10                  15

        Ile Ser Ser Gly Ser Cys Pro Phe Ser His Val Ser Gln Leu Ser Phe
                        20                  25                  30
30
        Ile Ala Thr Phe Ser Gln Ser Ser Pro Val Leu Leu Val Pro Ala Tyr
                    35                  40                  45

        Asn Thr Tyr Leu Ser Phe Leu Ala Phe Leu Asp Cys Ala Ser Leu Thr
35              50                  55                  60

        Ser Thr Xaa
         65


40


        (2) INFORMATION FOR SEQ ID NO: 241:

                (i) SEQUENCE CHARACTERISTICS:
45                      (A) LENGTH: 69 amino acids
                        (B) TYPE: amino acid
                        (D) TOPOLOGY: linear
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

50      Met Ser Thr Phe Gln Leu Leu Leu Ile Leu Ala Gln Ser Thr Tyr
          1               5                  10                  15

        Lys Ile Lys Ser Lys Pro Leu His Met Thr Asn His Thr Leu Leu Asn
                    20                  25                  30
55
        Ser Pro Gly Leu Asn Pro Ser Ser Pro Thr Leu Asn Phe Lys Thr Gln
                    35                  40                  45

        Gln His Glu Ser Val Ser Tyr Ala Cys Cys His Met Arg Ser Leu His
60              50                  55                  60
```

```
His Ala Phe Ala Xaa
 65
```

5

```
(2) INFORMATION FOR SEQ ID NO: 242:

        (i) SEQUENCE CHARACTERISTICS:
10              (A) LENGTH: 44 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

15  Met Val Ser Val Val Leu Ile Phe Ser Phe Leu Ser Leu Thr Ile Ser
     1               5               10              15

    Thr Thr Ala Ser Ala Tyr Asn Gly Asn Asp Thr Gln Gly Trp Asn Asp
             20              25              30
20
    Lys Phe His Xaa Xaa Ser Val Lys Thr Gln Thr Xaa
             35              40
```

25

```
(2) INFORMATION FOR SEQ ID NO: 243:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 51 amino acids
30              (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

    Met Ile Ser Asp Ala Gly Ala Gly Phe Gly Val Phe Leu Leu Val Pro
35   1               5               10              15

    Arg Ala Gly His Cys Trp Gly Ala Gly Lys Pro Leu Pro Ser Cys Pro
             20              25              30

40  Ser Val Ala Ser Ile Pro Ser Trp Val Leu Pro Ser Phe Leu Glu Arg
             35              40              45

    Gly Arg Xaa
         50
```

45

```
(2) INFORMATION FOR SEQ ID NO: 244:

50      (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 43 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

55
    Met Val Gln Thr Ile Gln Asp Phe Leu Ser Leu Phe Ser Thr Pro Ile
     1               5               10              15

    Phe Leu Leu Leu Leu Met Phe Glu Thr Leu Ser Leu Ala Pro Ala Trp
60           20              25              30
```

492

```
Leu Lys Pro Leu Arg Val Thr Ser His Ser Xaa
         35                  40
```

(2) INFORMATION FOR SEQ ID NO: 245:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 61 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
Met Ile Leu Met Pro Gly Leu Gly Thr Ser Arg Gln Arg Ser Val Pro
 1               5                  10                  15

Phe Val Pro Thr Leu Asn Ala Ser Thr Pro Gly Ala Met Thr Gly Pro
              20                  25                  30

Thr Ala Thr Leu Thr Ser Cys Gln Trp Thr Thr Ala Cys Arg Val Ser
         35                  40                  45

Trp Ala Asn Gly Trp Thr Ser Leu Arg Thr Phe Arg Xaa
     50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO: 246:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 36 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
Met Ser His His Ala Gln Pro Arg Phe Leu Leu Ile Thr Met Leu Leu
 1               5                  10                  15

Gln Glu Ala Lys Pro Val Ser Asn Ile Pro His Leu Leu Glu Ser Trp
              20                  25                  30

Tyr Phe Gly Xaa
         35
```

(2) INFORMATION FOR SEQ ID NO: 247:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 33 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
Met Asn Ser Leu Phe Trp Met Ile Leu Leu Pro Val Ser Gln Asp Gln
 1               5                  10                  15

Val Val Glu Gly Leu Gln Gly Gly Phe Ser Gln Ile His Met Arg Ile
              20                  25                  30
```

```
Leu Arg Lys His Leu Xaa
        35
```

(2) INFORMATION FOR SEQ ID NO: 248:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 211 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
Met Ser Arg Ser Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala
 1               5              10                  15

Ala Ser Ile Tyr Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala
            20              25              30

Leu His Gln Gly Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile
            35              40              45

Leu Leu Lys Leu Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg
        50              55              60

Met Gln Asp Leu Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala
 65              70              75              80

Trp Val Ser Leu Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr
                85              90              95

Ile Phe Gln Glu Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu
            100             105             110

Asn Gly Gln Ala Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala
            115             120             125

Glu Gly Leu Leu Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu
        130             135             140

Thr Leu Val Asn Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro
145             150             155             160

Glu Val Thr Asn Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser
            165             170             175

His Pro Phe Ile Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg
            180             185             190

Leu Val Leu Gln Tyr Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser
        195             200             205

Gly Pro Xaa
    210
```

(2) INFORMATION FOR SEQ ID NO: 249:

494

```
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 548 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:


    Met Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro
     1               5                  10                  15


    Arg Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu
            20                  25                  30


    Ile Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu
            35                  40                  45


    Ala Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro
            50                  55                  60


    Met Leu Gln Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu
     65                  70                  75                  80


    Gln Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg
                    85                  90                  95


    Gln Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp
                    100                 105                 110


    Val Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg
            115                 120                 125


    Ala Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg
            130                 135                 140


    Ile Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu
     145                 150                 155                 160


    Glu Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe
                    165                 170                 175


    Glu Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln
                    180                 185                 190


    Ala Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys
            195                 200                 205


    Glu Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln
            210                 215                 220


    Leu Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr
     225                 230                 235                 240


    Glu Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu
                    245                 250                 255


    Ile Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr
                    260                 265                 270


    Arg Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu
            275                 280                 285
```

60

495

```
        Asn Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe
            290             295             300

 5      Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu
        305             310             315             320

        Gly Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp
                    325             330             335

10      Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His
                    340             345             350

        His Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala
                    355             360             365
15
        Tyr Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile
            370             375             380

20      Val Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile
        385             390             395             400

        Glu Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr
                    405             410             415

25      Gln Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp
                    420             425             430

        Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys
                    435             440             445
30
        Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe
            450             455             460

        Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu
35      465             470             475             480

        His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu
                    485             490             495

40      Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys
                    500             505             510

        Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn
            515             520             525
45
        Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala
            530             535             540

        Lys Pro Ser Xaa
50      545
```

(2) INFORMATION FOR SEQ ID NO: 250:

55
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 299 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

496

```
Met Thr Thr Val Pro Pro Ser Pro Arg Pro Met Ser Arg Pro Ser Glu
  1           5           10          15

Arg Asn Met Arg Arg Pro Arg Gly Pro Ser Pro Leu Pro Ala Ser Pro
          20          25          30

Arg Asn Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe
      35          40          45

Leu Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser
     50          55          60

Phe Gly Leu Phe Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr
 65          70          75          80

His Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu
             85          90          95

Leu Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr
          100         105         110

Trp Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro
         115         120         125

Ala Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala
     130         135         140

Leu Ala Lys Asn Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu
145         150         155         160

Gly Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala
             165         170         175

Ala Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn
         180         185         190

Pro Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile
         195         200         205

Gly Val Lys Ala Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser
     210         215         220

His Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys
225         230         235         240

Asn Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg
             245         250         255

Phe Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala
         260         265         270

Glu Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu
     275         280         285

Tyr Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu
    290         295
```

497

(2) INFORMATION FOR SEQ ID NO: 251:

            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 40 amino acids
                   (B) TYPE: amino acid
                   (D) TOPOLOGY: linear
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Leu Leu Tyr Leu Leu Lys Val Xaa Val Ile Phe Val Phe Ser Ser Ser
 1   5   10   15

Lys Gly Val Thr Leu Val Ser Met Asn Leu Thr Ser Phe Phe Val Ser
         20   25   30

Ser Val Leu Ala Cys Phe Ser Xaa
         35   40

(2) INFORMATION FOR SEQ ID NO: 252:

            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 594 amino acids
                   (B) TYPE: amino acid
                   (D) TOPOLOGY: linear
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Met Pro Ala Ser Ser Leu Glu Ser Arg Ser Phe Leu Leu Ala Lys Lys
 1   5   10   15

Ser Gly Glu Asn Val Ala Lys Phe Ile Ile Asn Ser Tyr Pro Lys Tyr
         20   25   30

Phe Gln Lys Asp Ile Ala Glu Pro His Ile Pro Cys Leu Met Pro Glu
         35   40   45

Tyr Phe Glu Pro Gln Ile Lys Asp Ile Ser Glu Ala Ala Leu Lys Glu
         50   55   60

Arg Ile Glu Leu Arg Lys Val Lys Ala Ser Val Asp Met Phe Asp Gln
 65   70   75   80

Leu Leu Gln Ala Gly Thr Thr Val Ser Leu Glu Thr Thr Asn Ser Leu
             85   90   95

Leu Asp Xaa Leu Cys Tyr Tyr Gly Asp Gln Glu Pro Ser Thr Asp Tyr
             100   105   110

His Phe Gln Gln Thr Gly Gln Ser Glu Ala Leu Glu Glu Glu Asn Asp
         115   120   125

Glu Thr Ser Arg Arg Lys Ala Gly His Gln Phe Gly Val Thr Trp Arg
         130   135   140

Ala Lys Asn Asn Ala Glu Arg Ile Phe Ser Leu Met Pro Glu Lys Asn
145   150   155   160

Glu His Ser Tyr Cys Thr Met Ile Arg Gly Met Val Lys His Arg Ala
             165   170   175